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(54) Title: LIBRARIES OF EXPRESSIBLE GENE SEQUENCES (57) Abstract The invention described herein comprises libraries of expressible gene sequences. Such gene sequences are contained on plasmid vectors designed to endow the expressed proteins with a number of useful features such as affinity purification tags, epitope tags, and the like. The expression vectors containing such gene sequences can be used to transfect cells for the production of recombinant proteins. A further aspect of the invention comprises methods of identifying binding partners for the products of such expressible gene sequences.		

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LIBRARIES OF EXPRESSIBLE GENE SEQUENCES

RELATED APPLICATIONS

This application relies for priority on U.S. Provisional Application No. 60/080,626, filed April 3, 1998, and U.S. Provisional Application No. 60/096,981, filed August 18, 1998, each of which is hereby incorporated herein in its entirety.

Field of the Invention

The invention disclosed herein relates to the fields of genomics and molecular biology. More specifically the invention relates to libraries of expressible gene sequences and recombinant cells transfected therewith.

Background of the Invention

Recent breakthroughs in nucleic acid sequencing technology have made possible the sequencing of entire genomes from a variety of organisms, including humans. The potential benefits of a complete genome sequence are many, ranging from applications in medicine to a greater understanding of evolutionary processes. These benefits cannot be fully realized, however, without an understanding of how and where these newly sequenced genes function.

Traditionally, functional understanding started with recognizing an activity, isolating a protein associated with that activity, then identifying and isolating the gene, or genes, encoding that protein. Each gene of interest was identified, isolated and expressed separately, a relatively time consuming process.

Recently, breakthroughs in high through-put DNA sequencing technology have allowed massive amounts of gene sequence information to become available to the public. Yet methods of expressing these sequences to produce the proteins encoded by them for study have still required that each sequence be manipulated one at a time. Accordingly, a need exists for large numbers of expressible gene sequences.

The invention described herein addresses this and related needs as will become apparent upon inspection of the specification and the appended claims.

Brief Description of the Invention

The present invention comprises libraries of expressible gene sequences. Such
5 gene sequences are contained on plasmid vectors designed to endow the expressed proteins with a number of useful features such as affinity purification tags, epitope tags, and the like. The expression vectors containing such gene sequences can be used to transfect cells for the production of recombinant proteins.

A further aspect of the invention comprises methods of identifying binding
10 partners for the products of such expressible gene sequences.

Brief Description of the Figures

Figure 1 shows a schematic representation of the vaccinia topoisomerase type I cloning method used in the practice of the invention method.

Detailed Description of the Invention

15 The present invention comprises libraries of expressible gene sequences. Such gene sequences are contained on expression vectors which can be useful for transfecting cells and producing recombinant proteins. The expression vectors may additionally contain sequences that will endow the expressed proteins with a variety of useful features, such as peptides that aid in purification, epitope tags useful in
20 identifying recombinant protein, and the like.

The libraries of the invention are created by employing a high through-put methodology comprised of several steps. In the first step, the gene sequences that are to be expressed are amplified. By "amplification" it is meant that the copy number of the gene sequence(s) is increased. One commonly used method of amplification is the
25 polymerase chain reaction (PCR). In brief, starter DNA is heat-denatured into single strands. Two synthetic oligonucleotides, one complementary to sequence at the 3'

end of the sense strand of DNA segment of interest and the other complementary to the sequence at the 3' end of the anti-sense strand of a DNA segment of interest, are added in excess to the DNA sequence to be amplified and the temperature is lowered to 50 - 60° C. The specific oligonucleotides hybridize with the complementary
5 sequences in the DNA and then serve as primers of DNA chain synthesis, which requires the addition of a supply of deoxynucleotides and a temperature-resistant DNA polymerase, such as Taq polymerase, which can extend the primers at temperatures up to 72° C. When synthesis is complete, the whole mixture is heated further (up to 95° C) to melt the newly formed DNA duplexes. When the temperature
10 is lowered again, another round of synthesis takes place, since an excess of primer should still be present. Repeated cycles of synthesis and melting quickly amplify the sequence of interest. A more detailed description of PCR can be found in Erlich, Ed, *PCR Technology: Principles and Applications for DNA Amplification*, W.H. Freeman and Co., 1992 and Erlich, et al., Eds, *Polymerase Chain Reaction*, Cold Spring Harbor
15 Laboratory, 1989, both of which are incorporated by reference herein.

Starter DNA can come from a variety of sources. It can be total genomic DNA from an organism, for example, or can be cDNA that has been synthesized from cellular mRNA using reverse transcriptase. Genomic DNA and cDNA are distinguished in that genomic DNA contains introns, DNA which is spliced out during
20 post-transcriptional RNA processing and cDNA does not. Sources of suitable RNA include normal and diseased tissues, cellular extracts, and the like.

The desired gene sequences can come from any source. The examples presented below show the amplification of all open reading frames (ORFs) from a single organism, *Saccharomyces cerevisiae*, for example. By "open reading frame" it
25 is meant a segment of DNA that exists between a start codon and a stop codon and is likely to represent a gene. An open reading frame is also sometimes called a coding region to indicate that it contains only those nucleic acids that actually encode a protein. The examples presented below further show the amplification of a group of human genes thought to be important in the development of cancer.

Public databases exist that contain the entire or partial genome of a particular organism, for example yeast (*Saccharomyces cerevisiae*), prokaryotes (*Bacillus subtilis*, *E. coli*, *Borrelia burgdorferi*, *Helicobacter pylori*, *Mycoplasma genitalium*, and the like), fish (*Fugu rubripes*), mammals (human, mouse), plants (rice, cotton) and the like. Well known databases include GenBank, Unigene, EMBL, IMAGE and TIGR, for example. Public databases such as these can be used a source of gene sequences for use in the method of the invention. Such DNA sequence databases generally give each unique sequence an identifying number, such as a GenBank accession number. Generally, the organization creating and maintaining the database provides software tools for searching the database files for a particular record, such as by accession number, name, or sequence.

The primers employed in the amplification step are specific for each desired gene sequence and include a variety of unique features. For example, the 5' "sense" primer starts with the sequence 5'-CACCATG... (the start codon is underlined). The CACC sequence is added as a Kozak consensus that aids in translational efficiency. When the gene sequence being amplified represents a full-length gene, the 3' "antisense" codon is designed to make the amplification product end at the 3rd position of the last codon of the gene being amplified, plus a single adenine residue. This facilitates the fusion of the coding region in-frame with a heterologous peptide sequence such as an epitope tag, an affinity purification tag, and the like (see below). The sequence specific primers used in the practice of the invention are designed to prime sequence between the start and stop codon of an open reading frame. The use of such primers will produce a specific coding region that can be further processed according to the methods disclosed herein. Methods of designing sequence specific primers are well known in the art.

The gene sequence need not encode a full-length sequence, however, as the invention methods are equally suitable for any gene sequence, including Expressed Sequence Tags (ESTs). The primers can be synthesized and dried in multiwell

formats, such as 96-well microtiter plates to facilitate identification and further processing.

The amplified gene products are next isolated from the other components of the amplification reaction mixture. This purification can be accomplished using a variety of methodologies such as column chromatography, gel electrophoresis, and the like. A preferred method of purification utilizes low-melt agarose gel electrophoresis. The reaction mixture is separated and visualized by suitable means, such as ethidium bromide staining. DNA bands that represent correctly sized amplification products are cut away from the rest of the gel and placed into appropriate corresponding wells of a 96-well microtiter plate. These plugs are subsequently melted and the DNA contained therein utilized as cloning inserts. The use of gel electrophoresis has the advantage that the practitioner can purify the desired amplified gene sequence while additionally verifying that the sequence is of the correct size, i.e., represents the entire desired gene sequence.

The purified, amplified gene sequences are next inserted into an expression vector. A variety of expression vectors are suitable for use in the practice of the present invention, both for prokaryotic expression and eukaryotic expression. In general, the expression vector will have one or more of the following features: a promoter-enhancer sequence, a selection marker sequence, an origin of replication, an affinity purification tag sequence, an inducible element sequence, an epitope-tag sequence, and the like.

Promoter-enhancer sequences are DNA sequences to which RNA polymerase binds and initiates transcription. The promoter determines the polarity of the transcript by specifying which strand will be transcribed. Bacterial promoters consist of consensus sequences, -35 and -10 nucleotides relative to the transcriptional start, which are bound by a specific sigma factor and RNA polymerase. Eukaryotic promoters are more complex. Most promoters utilized in expression vectors are transcribed by RNA polymerase II. General transcription factors (GTFs) first bind specific sequences near the start and then recruit the binding of RNA polymerase II.

In addition to these minimal promoter elements, small sequence elements are recognized specifically by modular DNA-binding/trans-activating proteins (eg. AP-1, SP-1) which regulate the activity of a given promoter. Viral promoters serve the same function as bacterial or eukaryotic promoters and either provide a specific RNA
5 polymerase in trans (bacteriophage T7) or recruit cellular factors and RNA polymerase (SV40, RSV, CMV). Viral promoters are preferred as they are generally particularly strong promoters.

Promoters may be, furthermore, either constitutive or, more preferably, regulatable (i.e., inducible or derepressible). Inducible elements are DNA sequence
10 elements which act in conjunction with promoters and bind either repressors (eg. lacO/LAC Iq repressor system in *E. coli*) or inducers (eg. gal1/GAL4 inducer system in yeast). In either case, transcription is virtually "shut off" until the promoter is derepressed or induced, at which point transcription is "turned-on".

Examples of constitutive promoters include the int promoter of bacteriophage
15 λ , the bla promoter of the β -lactamase gene sequence of pBR322, the CAT promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage (P_L and P_R), the trp, reca, lacZ, LacI, AraC and gal promoters of *E. coli*, the α -amylase (Ulmanen et al., J. Bacteriol. 162:176-182, 1985)
20 and the sigma-28-specific promoters of *B. subtilis* (Gilman et al., Gene sequence 32:11-20(1984)), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY (1982)), *Streptomyces* promoters (Ward et al., Mol. Gen. Genet. 203:468-478, 1986), and the like. Exemplary prokaryotic promoters are reviewed by Glick (J. Ind. Microbiol. 1:277-
25 282, 1987); Cenatiempo (Biochimie 68:505-516, 1986); and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer et al., J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the

SV40 early promoter (Benoist et al., Nature (London) 290:304-310, 1981); the yeast
gal1 gene sequence promoter (Johnston et al., Proc. Natl. Acad. Sci. (USA)
79:6971-6975, 1982); Silver et al., Proc. Natl. Acad. Sci. (USA) 81:5951-5955,
1984), the CMV promoter, the EF-1 promoter, Ecdysone-responsive promoter(s), and
5 the like.

Selection marker sequences are valuable elements in expression vectors as
they provide a means to select, for growth, only those cells which contain a vector.
Such markers are of two types: drug resistance and auxotrophic. A drug resistance
marker enables cells to detoxify an exogenously added drug that would otherwise kill
10 the cell. Auxotrophic markers allow cells to synthesize an essential component
(usually an amino acid) while grown in media which lacks that essential component.

Common selectable marker gene sequences include those for resistance to
antibiotics such as ampicillin, tetracycline, kannamycin, bleomycin, streptomycin,
hygromycin, neomycin, Zeocin™, and the like. Selectable auxotrophic gene
15 sequences include, for example, hisD, which allows growth in histidine free media in
the presence of histidinol.

A preferred selectable marker sequence for use in yeast expression systems is
URA3. Laboratory yeast strains carrying mutations in the gene which encodes
orotidine-5'-phosphate decarboxylase, an enzyme essential for uracil biosynthesis, are
20 unable to grow in the absence of exogenous uracil. A copy of the wild-type gene
(ura4+ in *S. pombe* and URA3 in *S. cerevisiae*) will complement this defect in trans.

A further element useful in an expression vector is an origin of replication
sequence. Replication origins are unique DNA segments that contain multiple short
repeated sequences that are recognized by multimeric origin-binding proteins and
25 which play a key role in assembling DNA replication enzymes at the origin site.
Suitable origins of replication for use in expression vectors employed herein include
E. coli oriC, 2μ and ARS (both useful in yeast systems), sf1, SV40 (useful in
mammalian systems), and the like.

Additional elements that can be included in an expression vector employed in accordance with the present invention are sequences encoding affinity purification tags or epitope tags. Affinity purification tags can be generally peptide sequences that can interact with a binding partner immobilized on a solid support. Synthetic DNA sequences encoding multiple consecutive single amino acids, such as histidine, when fused to the expressed protein, may be used for one-step purification of the recombinant protein by high affinity binding to a resin column, such as nickel sepharose. An endopeptidase recognition sequence can be engineered between the polyamino acid tag and the protein of interest to allow subsequent removal of the leader peptide by digestion with Enterokinase, and other proteases. Sequences encoding peptides such as the chitin binding domain (which binds to chitin), glutathione-S-transferase (which binds to glutathione), biotin (which binds to avidin and streptavidin), and the like can also be used for facilitating purification of the protein of interest. The affinity purification tag can be separated from the protein of interest by methods well known in the art, including the use of inteins (protein self-splicing elements, Chong, et al, Gene 192:271-281, 1997).

Epitope tags are short peptide sequences that are recognized by epitope specific antibodies. A fusion protein comprising a recombinant protein and an epitope tag can be simply and easily purified using an antibody bound to a chromatography resin. The presence of the epitope tag furthermore allows the recombinant protein to be detected in subsequent assays, such as Western blots, without having to produce an antibody specific for the recombinant protein itself. Examples of commonly used epitope tags include V5, glutathione-S-transferase (GST), hemagglutinin (HA), the peptide Phe-His-His-Thr-Thr, chitin binding domain, and the like.

A further useful element in an expression vector is a multiple cloning site or polylinker. Synthetic DNA encoding a series of restriction endonuclease recognition sites is inserted into a plasmid vector downstream of the promoter element. These sites are engineered for convenient cloning of DNA into the vector at a specific position.

The foregoing elements can be combined to produce expression vectors useful in creating the libraries of the invention. Suitable prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (for example, pBR322, ColEI, pSC101, PACYC 184, pVX, pRSET, pBAD (Invitrogen, Carlsbad, CA) and the like).

- 5 Such plasmids are disclosed by Sambrook (cf. "Molecular Cloning: A Laboratory Manual", second edition, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, (1989)). *Bacillus* plasmids include pCI94, pC221, pTI27, and the like, and are disclosed by Gryczan (In: *The Molecular Biology of the Bacilli*, Academic Press, NY (1982), pp. 307-329). Suitable *Streptomyces* plasmids include
- 10 pIJ101 (Kendall et al., *J. Bacteriol.* 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater et al., In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary (1986), pp. 45-54). *Pseudomonas* plasmids are reviewed by John et al. (*Rev. Infect. Dis.* 8:693-704, 1986), and Izaki (*Jpn. J. Bacteriol.* 33:729-742, 1978).

- 15 Suitable eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, pcDNA3.1, pcDNA3.1/GS, pYES2/GS, pMT, pIND, pIND(Sp1), pVgRXR (Invitrogen), and the like, or their derivatives. Such plasmids are well known in the art (Botstein et al., *Miami Wntr. Symp.* 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance",
- 20 Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, *Cell* 28:203-204, 1982; Dillon et al., *J. Clin. Hematol. Oncol.* 10:39-48, 1980; Maniatis, In: *Cell Biology: A Comprehensive Treatise*, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980.

- Construction of chimaeric DNA molecules *in vitro* relies traditionally on two
- 25 enzymatic steps catalyzed by separate protein components. PCR amplification or site-specific restriction endonucleases are used to generate linear DNAs with defined termini that can then be joined covalently at their ends via the action of DNA ligase. DNA ligase has limitations, however, in that it is relatively slow acting and temperature sensitive.

Thus, when inserting the purified, amplified gene sequence into the expression vector the use of an enzyme that can both cleave and religate DNA in a site specific manner is preferred. Any site-specific enzyme of this type is suitable, for example, a type I topoisomerase or a site-specific recombinase. Examples of suitable site-specific recombinases include lambda integrase, FLP recombinase, P1-Cre protein, Kw recombinase, and the like (Pan, et al, J. Biol. Chem. 268:3683-3689, 1993; Nunes-Duby, et al, EMBO J. 13:4421-4430, 1994; Hallet and Sherratt, FEMS Microbio. Revs 21:157-178, 1997; Ringrose, et al, Eur J. Biochem 248:903-912, 1997).

A particularly suitable enzyme for use in creating the libraries of the invention is a type I topoisomerase, particularly vaccinia DNA topoisomerase. Vaccinia DNA topoisomerase binds to duplex DNA and cleaves the phosphodiester backbone of one strand. The enzyme exhibits a high level of sequence specificity, akin to that of a restriction endonuclease. Cleavage occurs at a consensus pentapyrimidine element 5'-(C/T)CCTT in the scissile strand. In the cleavage reaction, bond energy is conserved via the formation of a covalent adduct between the 3' phosphate of the incised strand and a tyrosyl residue of the protein. Vaccinia topoisomerase can religate the covalently held strand across the same bond originally cleaved (as occurs during DNA relaxation) or it can religate to a heterologous acceptor DNA and thereby create a recombinant molecule.

When the substrate is configured such that the scissile bond is situated near (within 10 basepairs of) the 3' end of a DNA duplex, cleavage is accompanied by the spontaneous dissociation of the downstream portion of the cleaved strand. The resulting topoisomerase-DNA complex, containing a 5' single-stranded tail, can religate to an acceptor DNA if the acceptor molecule has a 5' OH tail complementary to that of the activated donor complex.

In accordance with the present invention, this reaction has been optimized for joining PCR-amplified DNA fragments into plasmid vectors (See Figure 1). PCR fragments are naturally good surrogate substrates for the topoisomerase I religation

step because they generally have 5' hydroxyl residues from the primers used for the amplification reaction. The 5' hydroxyl is the substrate for the religation reactions. The use of vaccinia topoisomerase type I for cloning is described in detail in copending US patent application serial number 08/358,344, filed 12/19/94,
5 incorporated by reference herein in its entirety.

The gene sequence being inserted into the expression vector can insert in either the sense or antisense direction. Therefore, the creation of a useful library should include verification of both the size and orientation of the insert to insure that the gene sequence will express the desired protein. Preferably, the insert plus vector
10 is utilized in a standard bacterial transformation reaction and the contents of the transformation plated onto a selective growth media. Bacterial transformation and growth selection procedures are well known in the art and described in detail in, for example, Ausubel, et al, Short Protocols in Molecular Biology, 3rd ed. 1995.

Individual bacterial colonies are picked and grown in individual wells of a 96
15 well microtiter plate containing selective growth media. An aliquot of these cells is used directly in a diagnostic PCR reaction. Primers for this reaction are designed such that only plasmids with correctly oriented inserts give amplification product. The amplified DNA is separated and visualized by SDS-PAGE gel electrophoresis using standard protocols (see Ausubel, et al, Short Protocols in Molecular Biology, 3rd ed.
20 1995).

Performing the PCR reaction directly from the cultured cell lysates, rather than first preparing DNA from the bacteria, is a particular advantage as it significantly reduces both the time needed to generate the required data and the cost of doing so.

Once plasmids containing the gene sequence insert in the correct orientation
25 have been identified, plasmid DNA is prepared for use in the transformation of host cells for expression. Methods of preparing plasmid DNA and transformation of cells are well known to those skilled in the art. Such methods are described, for example, in Ausubel, et al, supra.

Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other organisms may also be used, including other bacterial strains.

5 Recognized prokaryotic hosts include bacteria such as *E. coli* and those from genera such as *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host selected for use herein must be compatible with the replicon and control sequences in the expression plasmid.

10 Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, and mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO, 3T3 or CHOK1, HEK 293 cells or cells of lymphoid origin (such as 32D cells) and their derivatives. Preferred mammalian host
15 cells include nonadherent cells such as CHO, 32D, and the like. Preferred yeast host cells include *S. pombe*, *Pichia pastoris*, *S. cerevisiae* (such as INVSc1), and the like.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, nopaline synthase promoter and polyadenylation signal sequences, and the like.

20 Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used. Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of peptide encoded by a desire gene sequence in insects cells (Jasny, Science 238:1653, 1987); Miller et al., In: Genetic Engineering
25 (1986), Setlow, J.K., et al., eds., Plenum, Vol. 8, pp. 277-297). The present invention also features the purified, isolated or enriched versions of the expressed gene products produced by the methods described above.

Kits comprising one or more containers or vials containing components for using the libraries of the present invention are also within the scope of the invention. Kits can comprise any one or more of the following elements: one or more expressible gene sequences, cells which are, or can be, transfected with such gene sequences, and antibodies recognizing the expressed gene product or an epitope tag associated therewith. Cells suitable for inclusion in such a kit include bacterial cells, yeast cells (such as INVSc1), insect cells or mammalian cells (such as CHO).

In one embodiment, such a kit comprises a detergent solution, preferably the Trax® lysing reagent (6% NP-40 and 9% Triton X-100 in 1X PBS). Also included in the kit can be one or more binding partners, *e.g.*, an antibody or antibodies, preferably a pair of antibodies to the same expressed gene product, which preferably do not compete for the same binding site on the expressed gene product.

In another embodiment, a kit comprises more than one pair of such antibodies or other binding partners, each pair directed against a different target molecule, thus allowing the detection or measurement of a plurality of such target molecules in a sample. In a specific embodiment, one binding partner of the kit may be pre-adsorbed to a solid phase matrix, or alternatively, the binding partner and matrix are supplied separately and the attachment is performed as part of the assay procedure. The kit preferably contains the other necessary washing reagents well-known in the art. For EIA, the kit contains the chromogenic substrate as well as a reagent for stopping the enzymatic reaction when color development has occurred. The substrate included in the kit is one appropriate for the enzyme conjugated to one of the antibody preparations. These are well-known in the art. The kit can optionally also comprise a target molecule standard; *i.e.*, an amount of purified target molecule that is the target molecule being detected or measured.

In a specific embodiment, a kit of the invention comprises in one or more containers: (1) a solid phase carrier, such as a microtiter plate coated with a first binding partner; (2) a detectably labeled second binding partner which binds to the same expressed gene product as the first binding partner; (3) a standard sample of the

expressed gene product recognized by the first and second binding partners; (4) concentrated detergent solution; and (5) optionally, diluent.

In another embodiment, the invention features methods of screening cells for binding partners of an expressed gene product of the invention. By "natural binding partner" it is meant a molecule that interacts specifically with the expressed gene product. Binding partners include ligands, agonists, antagonists and downstream signaling molecules such as adaptor proteins and may be identified by techniques well known in the art such as co-immunoprecipitation or by using, for example, a two-hybrid screen. (Fields and Song, U.S. Patent No. 5,283,173, issued February 1, 1994 and, incorporated by reference herein.).

Binding partners contemplated by the invention may additionally be antibodies. The term "antibody" is used herein in the broadest sense and specifically includes intact monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g. bispecific antibodies) formed from at least two intact antibodies, and antibody fragments, including single chain antibodies, so long as they exhibit the desired binding properties as described herein.

Various procedures well-known in the art may be used for the production of polyclonal antibodies to an epitope or antigen of interest. A host animal of any of a number of species, such as rabbit, goat, sheep, horse, cow, mice, rat, etc. is immunized by injection with an antigenic preparation which may be derived from cells or microorganisms, or may be recombinantly or synthetically produced. Various adjuvants well known in the art may be used to enhance the production of antibodies by the immunized host, for example, Freund's adjuvant (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, liposomes, potentially useful human adjuvants such as BCG (Bacille Calmette-Guerin) and *Propionibacterium acnes*, and the like.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. Preferred antibodies are mAbs, which may be of any immunoglobulin class including IgG, IgM, IgE, IgA, and any subclass or isotype thereof.

In addition to their specificity, monoclonal antibodies are advantageous in that they are synthesized by hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.*, *Nature*, 256:495 (1975), or may be made by recombinant DNA methods (see, *e.g.*, U.S. Patent No. 4,816,567, incorporated by reference herein). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.*, *Nature*, 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991), for example.

The monoclonal antibodies contemplated for use herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as

they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:6851-6855 (1984)).

“Humanized” forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementarity-determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues which are not found in either the recipient antibody or in the imported CDR or framework sequences. These modifications are made to further refine and maximize antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, *Nature*, 321:522-525 (1986); Reichmann *et al.*, *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992). The humanized antibody includes a PRIMATIZED™ antibody wherein the antigen-binding region of the antibody is derived from an antibody produced by immunizing macaque monkeys with the antigen of interest.

“Antibody fragments” comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies

(Zapata *et al. Protein Eng.* 8(10):1057-1062 (1995)); single-chain antibody molecules, multispecific antibodies formed from antibody fragments, and the like.

Particularly preferred in the practice of the invention are single-chain antibodies. "Single-chain" or "sFv" antibodies are antibody fragments comprising the

5 V_H and V_L domains of an antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFvs see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore Eds.,

10 Springer-Verlag, New York, pp. 269-315 (1994).

Large quantities of single chain antibodies with uncharacterized randomized binding specificity can be produced using a number of methodologies known in the art. Random peptide libraries can be created in filamentous phage particles (Daniels and Lane, *Methods* 9(3):494-507, 1996; Reichmann and Weill, *Biochemistry*

15 32(34):8848-8855; Rader and Barbas, *Curr Opin Biotechnol* 9(4):503-508, 1997; Iba and Kurosawa, *Immunol Cell Biol* 75(2):217-221, 1997), for example, or similarly in yeast, bacteria, and the like. Other methods for creating random libraries of sFvs include various solid state synthesis methods.

The term "diabodies" refers to small antibody fragments with two antigen-

20 binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain ($V_H - V_L$). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more

25 fully in, for example, EP 404,097; WO 93/11161; and Hollinger *et al., Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

Methods of identifying specific antibodies are well known in the art and include methods such as ELISAs, Western blots, immunoprecipitation, and the like

(see, for example, Ausubel, et al, Short Protocols in Molecular Biology, 3rd ed. 1995, incorporated herein in its entirety). One method of large scale, high through-put screening for specific antibodies is described in co-pending US application entitled Microarrays and Uses Therefor, filed Feb. 4, 1999, U.S. Serial No. 09/245,615.

- 5 The invention will now be described in greater detail by reference to the following non-limiting examples.

Examples -

Example 1 - High-throughput Expression of Yeast ORFs

- 10 The following example illustrates the creation of a library of expressible yeast gene sequences.

Amplification -

- 15 6,032 yeast ORFs and a corresponding gene-specific primer of the 3' end of each were obtained from Research Genetics (Huntsville, AL) in a 96-well microtiter plate format at a concentration of 0.3 ng/ μ l. Each gene specific primer was designed to exclude the gene's stop codon. Since the templates each contain a common sequence immediately 5' of the start ATG (5'-GCAGTCCTGGAATTCCAGCTGACCACC) (SEQ. ID. NO.: 1), each template could be amplified with a common 5' primer.

- 20 5 μ l of ORF template was added to a fresh 96-well microtiter plate (polycarbonate Thermowell Thinwall, Model M. Cat # 6511) using a 12 channel pipetter. 6 μ l of specific 3' primer solution (2 μ M) was added and the total volume per well brought to 30 μ l with PCR cocktail, immediately after which the plate was placed on ice. (PCR cocktail for 120 reactions - 720 μ l 5X Buffer J, 48 μ l dNTPs (50mM stock), 12 μ l common 5' primer (1 μ g/ μ l stock), 48 μ l Taq DNA polymerase (Boeringer-Mannheim or Promega, 5 units/ μ l), 1.92 μ l Pfu DNA polymerase (Stratagene, cat. # 600153-81, 2.5 units/ μ l) and 1464 μ l distilled water. 5X Buffer J:
- 25

300 mM Tris (pH 9.5), 75 mM ammonium sulfate, 10 mM MgCl_2). The rubber Hybaid Micromat lid was washed by soaking in 0.1 M HCl, then rinsed for 2 minutes with distilled water and dried completely before applying to the 96-well plate.

The PCR reaction was performed using a Hybaid, Ltd. (Middlesex, UK)

- 5 thermo-cycler according to the manufacturer's instructions. The conditions used were as follows: pre-melt step: 94° C x 4 min; melt step: 94° C x 30 sec, anneal step: 58° C x 45 sec, extend step: 72° C x 3 min - repeated for 25 cycles; final extension: 72° C x 4 min; final block temperature set to room temp (approx. 22° C). The plates were stored at 4° C.

10 Purification -

- The plates were spun briefly at 1000 rpm, then 10 μl of 6X gel loading dye was added to each well (6X gel loading dye: 6 mM Tris (pH 8), 6 mM EDTA, 0.03% Bromphenol Blue, 30% glycerol). The entire contents of each well were loaded onto a 1% low melt agarose (Invitrogen # 46-0150) gel (plus
15 ethidium bromide at 20 μl of a 10 mg/ml solution added to 400 mls of agarose) in 1X TAE (50X TAE = 242g Tris base, 57.1 ml glacial acetic acid, 100 ml 0.5 M EDTA, pH 8.0 per liter (water)) and run at 110 - 120 volts for 1.25 to 1.5 hours. A UV light box was used to visualize the amplification products and ensure that only correct-sized PCR products are used in the insertion step..

20 Insertion into expression vector(s) -

- The portion of each lane containing the amplified gene sequence was cut from the gel and transferred to a well in a 96-well microtiter plate, melted on a heat block (75° C), and a portion of the melt multi-channel pipetted into a 96-well microtiter plate (7 μl /well) containing one of two expression vectors: TOPO-adapted
25 pcDNA3.1/GS or pYES2/GS (see Example 3, below). The plate was covered with parafilm and incubated at 37° C for 7 minutes. Top 10 Chemically Competent Cells (Invitrogen) were added to each well (45 μl /well, O.D.=4.7), whereupon the plate was re-covered and incubated on ice for 5 minutes. The cells were then heat shocked on a

42° C block for 1 minute and returned to ice for 1 minute. An aliquot of SOC medium was added to each well (150 µl, 20g tryptone, 5g yeast extract, 0.5g NaCl, 250 mM KCl, 20 ml 1M glucose/liter), and the plate was incubated at 37° C for 90 to 120 minutes.

- 5 The contents of each well were plated onto a LB(10g tryptone, 5g yeast extract, 10g NaCl per liter)/1.5% agar petrie plate containing the appropriate selection marker (ampicillin (50 µg/ml) for pYES2/GS and Zeocin™ (25 µg/ml) for pcDNA3.1/GS). The petrie plates were grown overnight at 37° C.

Verification of size and orientation -

- 10 Contamination is a potentially serious problem in this step. Care should be taken to guard against contaminating the process through airborne contamination, unsterile reagents or equipment, or well-to-well contamination.

- Eight colonies were picked from each petrie plate and placed in eight individual wells of a 96-well microtiter plate. Each well contained 100 µl of 2X LB
15 plus 100 µg/ml ampicillin or 50 µg/ml Zeocin™ as appropriate for the expression vector used. The plates were incubated overnight at 37° C.

- The plates were spun briefly at 1000 rpm. The cells were stirred by pipetting up and down in a pipetter, then 2 µl from each well was transferred to a corresponding well in a PCR reaction plate containing 28 µl/well PCR cocktail (PCR cocktail for 840
20 reactions - 5040 µl 5X Buffer J, 336 µl dNTPs (50mM stock), 84 µl common 5' primer (1 µg/µl stock, Dalton Chemical Lab. Inc, Ont. CAN), 84 µl 3' H6stopprevu primer (1 µg/µl, Dalton Chemical Lab. Inc, Ont. CAN), 336 µl Taq DNA polymerase (Boeringer Mannheim or Promega 5 units/µl), and 17.64 mls distilled water.
H6stopprevu primer has the sequence 5' AAA CTC AAT GGT GAT GGT GAT GAT
25 GACC - 3') (SEQ. ID. NO.: 2).

 The PCR reaction was run essentially as described above with the following cycle: pre-melt step: 94° C x 10 min; melt step: 94° C x 1 min, anneal step: 67° C x

1 min, extend step: 72° C x 3 min - 35 cycles; final extension: 72° C x 4 min; final block temp set to room temp (approximately 22° C). The plates were spun briefly at 100 rpm and 6 µl of 6X gel loading dye added to each well. Samples were run on a 1% agarose gel which was subsequently stained with ethidium bromide. Only
5 plasmids with correctly oriented inserts give an amplification product in this step.

The location of the positive clones was entered into a database and a spreadsheet of positive clones generated. The spreadsheet was downloaded onto a Qiagen BioRobot 9600™ to direct the re-racking of the positive cultures into deep-well culture blocks. Essentially, a single positive culture for each clone was grown
10 and used to prepare plasmid DNA according to the Quia-Prep Turbo protocol.

CHO cells or were transfected with the prepared plasmid DNA using the Pfx-6 PerFect Lipid system (Invitrogen, Cat #T930-16). Yeast cells (INVSc1) were transfected using the S.C. EasyComp Transformation kit (Invitrogen, Cat #K5050-01). Expression was verified by Western blot using anti-V5 antibody to detect the
15 epitope tag. All of the yeast ORFs were expressed in either pYES or pDNA3.1. Table 1 below lists the yeast proteins successfully produced using the yeast ORFs.

Table 1 Yeast ORFs

Plate Name	ORF Identifier	Protein description			
M12 E2	YAL003W	447-987 Translation elongation factor EF-1beta GDPVGTP exchange factor for Tef1pVTef2p (22.77/40)	M12 F5	YAL015C	DNA glycosylase (43.92/48)
			M12 D6	YAL016W	protein phosphatase 2A regulatory subunit A (69.96/56)
M12 D4	YAL005C	Heat shock protein of HSP70 family cytoplasmic (70.65/45)	M136 H1	YAL020C	(36.66/47)
M12 E5	YAL007C	(23.68/32)	M12 F4	YAL022C	(56.90/56)
M11 H1	YAL009W	Protein required for meiosis (28.60/30)	M11 E4	YAL030W	216-467 vesicle-associated membrane protein (synaptobrevin) homolog (12.98/20)
M135 F2	YAL012W	cystathionine gamma-lyase (43.45/43)	M136 D1	YAL034W -A	(31.9/28)
M11 D2	YAL013W	(39.93/40)	M12 H5	YAL037W	(29.48/33)
M11 E2	YAL014C	(22.58/31)	M136 H4	YAL038W	Pyruvate kinase (55.11/60)

M136 G5	YAL039C	cytochrome c heme lyase (CCHL) (29.62/45)
M136 C4	YAL044C	H-protein subunit of the glycine cleavage system (19.50/36)
M12 G6	YAL045C	(11.25/11)
M11 C7	YAL049C	(27.09/37)
M135 H4	YAL053W	(86.24/64)
M136 B5	YAL055W	(19.91/28)
M12 G7	YAL056W	(93.28/98)
M12 B3	YAL059W	(23.43/34)
M11 D8	YAL060W	(42.13/45)
M12 A5	YAL061W	(45.98/40)
M11 F8	YAL062W	(50.48/50)
M11 H9	YAR002W	(59.4/60)
M12 F1	YAR003W	(46.97/53)
M12 C3	YAR008W	34kDa subunit of the tetrameric tRNA splicing endonuclease (30.46/38)
M12 B5	YAR010C	(48.43/45)
M11 C11	YAR023C	(19.72/30)
M12 B4	YAR027W	(25.96/40)
M12 C5	YAR028w	(25.85/30)
M12 B7	YAR030C	(12.46/12)
M135 E2	YAR035W	Outer carnitine acetyltransferase mitochondrial (75.68/76)
M12 E3	YAR037W	(21.34/25)
M12 C4	YAR040C	(13.12/20)
M138 E1	YAR052C	(13.89/36)
M14 F1	YAR062W	(21.89/36)
M138 H5	YBL001C	ExtraCellular Mutant (11.47/10)
M137 B1	YBL002W	Histone H2B (HTB1 and HTB2 code for nearly identical proteins) (14.52/25)
M14 B3	YBL003C	Histone H2A (HTA1 and HTA2 code for nearly identical proteins) (14.55/15)
M13 F3	YBL005W -A	(48.51/48)
M13 C2	YBL010C	(30.83/35)
M333 D1	YBL011W	(83.6/93)
M138 A6	YBL015W	acetyl CoA hydrolase (57.97/60)

M137 C1	YBL016W	cdc2+VCDC28 related kinase with positive role in conjugation (38.94/45)
M310 B1	YBL019W	(57.31/64)
M13 G3	YBL020W	67 kDa integral membrane protein (63.25/70)
M13 D4	YBL021C	transcriptional activator protein of CYC1 (15.87/20)
M13 G2	YBL027W	387-954 Ribosomal protein YL14 (rat L19) (rp33) (RPL19A and RPL19B code for identical genes) (20.9/32)
M137 C4	YBL028C	(11.69/20)
M137 G6	YBL031W	(37.29/38)
M14 B7	YBL033C	GTP cyclohydrolase II (37.98/38)
M137 D3	YBL035C	B subunit of DNA polymerase alpha-primase complex (77.58/80)
M13 H3	YBL036C	(28.30/32)
M138 C5	YBL038W	Mitochondrial ribosomal protein MRPL16 (25.63/30)
M137 B2	YBL041W	proteasome subunit (26.62/36)
M13 H2	YBL043W	ExtraCellular Mutant (28.48/45)
M13 A4	YBL044W	(13.53/17)
M13 C5	YBL046W	(48.62/55)
M138 F2	YBL050W	147-995 peripheral membrane protein required for vesicular transport between ER and Golgi (32.23/35)
M137 C2	YBL057C	(23.57/36)
M14 C10	YBL058W	isolated as a suppressor of the lethality caused by overexpression of the phosphoprotein phosphatase 1 catalytic subunits encoded by GLC7 (46.64/50)
M13 B4	YBL060W	(75.68/75)
M137 D1	YBL064C	(28.74/36)

M15 A1	YBL080C	62-kDa protein (59.54/60)
M141 C1	YBL081W	(40.59/60)
M16 F1	YBL082C	Resistance to Hansenula Killer 1 hypothetical F-458 protein (50.41/50)
M15 H5	YBL086C	(51.29/?)
M15 H4	YBL093C	nuclear protein (24.23/36)
M15 D7	YBL095W	(29.81/50)
M140 E3	YBL099W	mitochondrial F1F0- ATPase alpha subunit (60.06/60)
M15 B6	YBL101W -A	(48.29/48)
M310 C1	YBL105C	putative protein kinase (126.64/150)
M16 A3	YBL107C	(21.59/31)
M15 C4	YBR002C	(31.49/32)
M15 B5	YBR003W	hexaprenyl pyrophosphate synthetase (52.14/55)
M16 H3	YBR004C	(47.66/48)
M15 F7	YBR005W	(23.54/40)
M140 D4	YBR010W	Histone H3 (HHT1 and HHT2 code for identical proteins) (15.07/20)
M15 C5	YBR011C	Inorganic pyrophosphatase (31.60/50)
M15 E6	YBR012C	(15.32/18)
M15 G7	YBR012W -A	(48.51/64)
M15 A3	YBR014C	(22.46/22)
M15 E4	YBR016W	(14.19/14)
M15 F6	YBR018C	galactose-1-phosphate uridyl transferase (40.29/45)
M15 H7	YBR019C	UDP-glucose 4- epimerase (76.92/76)
M141 A3	YBR024W	(33.22/37)
M16 D3	YBR025C	(43.47/43)
M15 G6	YBR026C	Nuclear protein that binds to T-rich strand of core consensus sequence of autonomously replicating sequence (41.83/41)

M140 G3	YBR031W	large ribosomal subunit protein 2A (39.93/42)
M140 F6	YBR034C	protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme) (38.31/50)
M15 A8	YBR035C	pyridoxine (pyridoxiamine) phosphate oxidase (25.11/32)
M255 C1	YBR036C	contains 9 or 10 putative membrane spanning regions\ putative Ca ²⁺ binding protein (homology to EF- hand Ca ²⁺ binding site) (45.13/55)
M16 H1	YBR046C	(36.77/35)
M15 A7	YBR050C	(37.21/50)
M140 E1	YBR052C	(23.13/34)
M15 G5	YBR057C	Muddled Meiosis (40.29/70)
M19 B1	YBR061C	(34.13/40)
M143 A4	YBR063C	(44.47/48)
M143 C7	YBR066C	(24.23/25)
M19 A2	YBR068C	probable amino acid permease for leucine valine and isoleucine (67.02/67)
M19 C2	YBR070C	(26.10/40)
M143 B4	YBR071W	(23.32/33)
M142 E6	YBR072W	heat shock protein 26 (23.65/32)
M143 B2	YBR077C	(17.85/32)
M142 B5	YBR079C	(106.07/106)
M19 E3	YBR080C	cytoplasmic protein involved in protein transport between ER and Golgi\ ATPase(83.41/080)
M19 F3	YBR081C	transcription factor (146.55/050)
M19 G3	YBR082C	143-542 ubiquitin- conjugating enzyme (16.49/16)
M202 D1	YBR083W	transcriptional regulator of Ty1 expression (53.57/64)

M19 A4	YBR084C-A	509-1076 Ribosomal protein YL14 (rat L19) (rp33) (RPL19A and RPL19B code for identical genes) (20.9/?)
M19 C4	YBR085W	mitochondrial ADP/ATP translocator (33.88/50)
M143 D6	YBR088C	proliferating cell nuclear antigen (28.41/0)
M19 A5	YBR090C-A	11-kDa nonhistone chromosomal protein (10.92/10)
M143 C2	YBR091C	(12.02/16)
M143 D3	YBR092C	Acid phosphatase constitutive (51.40/50)
M19 E5	YBR094W	(82.94/80)
M19 F5	YBR095C	(49.86/50)
M20 E1	YBR098W	(51.92/48)
M143 D4	YBR101C	(31.93/32)
M142 E10	YBR105C	(39.85/45)
M143 F1	YBR106W	May be a membrane protein involved in inorganic phosphate transport and regulation of Pho81p function (20.79/0)
M143 E4	YBR109C	Calmodulin(16.20/12)
M20 G7	YBR111C	(25.44/30)
M143 A8	YBR112C	General repressor of transcription (with Tup1p)\ mediates glucose repression (106.29/100)
M19 H7	YBR113W	(17.71/70)
M20 F6	YBR118W	translational elongation factor EF-1 alpha (50.49/55)
M19 F8	YBR119W	98-986 U1 snRNP A protein (32.89/36)
M143 B8	YBR120C	(17.85/36)
M19 H8	YBR121C	Glycyl-tRNA synthase (73.40/90)
M19 A9	YBR122C	Mitochondrial ribosomal protein MRPL36 (YmL36) (21.59/30)

M142 A3	YBR123C	transcription factor tau (TFIIIC) subunit 95 (71.42/75)
M19 E9	YBR126C	56 kD synthase subunit of trehalose-6-phosphate synthase/vphosphatase complex (54.48/55)
M19 F9	YBR127C	(56.90/36)
M20 D9	YBR128C	(37.87/37)
M143 B9	YBR129C	(36.11/40)
M19 A10	YBR130C	(46.78/50)
M143 E2	YBR131W	(77.55/72)
M19 F10	YBR135W	subunit of the Cdc28 protein kinase (16.61/16)
M143 C9	YBR137W	(19.8/30)
M143 F2	YBR139W	(55.99/0)
M20 E9	YBR144C	(11.47/32)
M19 A12	YBR146W	Probable mitochondrial ribosomal protein S9 (30.69/31)
M265 B1	YBR149W	(37.95/40)
M20 F9	YBR152W	(32.12/50)
M19 H12	YBR153W	Protein involved in the biosynthesis of riboflavin second step in the riboflavin biosynthesis pathway (26.95/40)
M145 C4	YBR158W	(60.5/98)
M144 B9	YBR161W	(41.47/52)
M144 B1	YBR162C	(50.08/60)
M145 B2	YBR162W-A	Protein that participates in secretory pathway (7.36/10)
M145 D4	YBR165W	(30.58/36)
M144 H6	YBR166C	Prephenate dehydrogenase (NADP+) (49.75/50)
M145 C1	YBR169C	Member of the 70-kDa heat-shock protein family (76.36/98)
M144 C3	YBR171W	integral membrane glycoprotein (22.77/32)
M145 E4	YBR173C	(16.31/35)
M144 D9	YBR176W	ExtraCellular Mutant (34.43/45)

M145 D1	YBR177C	(49.64/60)
M144 D3	YBR179C	Yeast fzo homolog (drosophila melanogaster fuzzy onions gene)Reference:Hales K.G. and Fuller M.T. -1997 Developmentally regulated mitochondrial fusion mitochondrial fusion mediated by a conserved novel predicted GTPase. Cell. 90 121-129. (94.08/98)
M144 H5	YBR181C	359-1063 40S ribosomal gene product S10 (26.07/32)
M145 F5	YBR182C	(49.75/0)
M144 E3	YBR187W	(30.91/36)
M144 E4	YBR188C	(15.43/20)
M144 A6	YBR189W	421-1001 Ribosomal protein SUP46/RPS13 (YS11A) (YP28) (E. coli S4) (rat S9)(21.56/33)
M144 F1	YBR193C	(24.56/34)
M144 F1	YBR193C	(24.56/34)
M145 F2	YBR194W	(13.64/20)
M144 F4	YBR196C	phosphoglucosyltransferase (60.97/60)
M144 B6	YBR197C	(23.90/32)
M145 E6	YBR199W	Putative alpha-1 2-mannosyltransferase (51.15/64)
M144 G9	YBR200W	contains two SH3 domains (60.72/64)
M144 G4	YBR204C	(41.38/38)
M144 C6	YBR205W	Putative alpha-1 2-mannosyltransferase (44.55/48)
M145 F1	YBR209W	(11.66/16)
M144 F2	YBR210W	(15.73/16)
M144 H4	YBR212W	negative growth regulatory protein (74.03/74)
M144 D6	YBR213W	(30.35/38)
M145 H5	YBR214W	(58.08/90)

M144 E6	YBR221C	beta subunit of pyruvate dehydrogenase (E1 beta) (40.39/42)
M202 E1	YBR222C	(59.76/70)
M145 A6	YBR230C	109-502(14.85/18)
M144 H8	YBR231C	(33.46/42)
M145 H1	YBR233W	(45.54/60)
M144 C5	YBR236C	RNA (guanine-7-methyltransferase (cap methyltransferase) (47.99/52)
M144 F6	YBR237W	RNA helicase homolog (93.5/95)
M144 H2	YBR242W	(26.39/32)
M255 D1	YBR243C	UDP-N-acetylglucosamine-1-P transferase (GPT) (49.31/38)
M145 B4	YBR244W	(17.93/0)
M144 A9	YBR247C	Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PAGE (53.26/55)
M144 D10	YBR248C	glutamine amidotransferase:cyclase (60.75/61)
M147 A1	YBR249C	3-deoxy-D-arabinoheptulosonate 7-phosphate (DAHP) synthase isoenzyme (40.73/50)
M24 C1	YBR251W	Probable mitochondrial ribosomal protein S5 (33.88/40)
M146 B4	YBR253W	transcription factor (13.42/18)
M146 D7	YBR256C	Riboflavin synthase alpha-chain (26.21/26)
M25 D1	YBR258C	(15.65/20)
M146 C4	YBR261C	(25.55/38)
M146 D5	YBR262C	(11.69/50)
M147 F6	YBR263W	Serine hydroxymethyltransferase mitochondrial (62.36/62)
M24 A3	YBR265W	(35.31/35)
M25 F1	YBR267W	(32.56/45)
M146 E5	YBR270C	(59.98/64)

M146 B1	YBR273C	(47.99/70m)
M146 F1	YBR274W	(58.08/50)
M303 C1	YBR283C	(53.93/48)
M146 F4	YBR285W	(15.95/30)
M24 B6	YBR290W	(35.42/55)
M25 G1	YBR291C	citrate transporter in mitochondrial inner membrane (32.92/35)
M274 D1	YBR295W	Putative P-type Cu(2+)-transporting ATPase (133.87/125)
M25 H1	YCL005W	(28.05/40)
M147 B7	YCL009C	Acetolactate synthase regulatory subunit (34.02/34)
M146 B5	YCL016C	(34.02/34)
M25 G3	YCL018W	beta-IPM (isopropylmalate) dehydrogenase (40.25/55)
M147 E8	YCL027W	MAP kinase involved in pheromone signal transduction G(sub)1 arrest (56.43/50)
M146 C2	YCL029C	Microtubule-associated protein required for microtubule function during mating and mitosis (48.43/70)
M147 E5	YCL032W	Protein that interacts with Gpa1p Ste4 and Ste18 to regulate adaptation to pheromone (38.27/48)
M146 D8	YCL035C	(12.13/16)
M147 F2	YCL037C	Suppressor of rho3 (51.39/55)
M146 C7	YCL042W	(13.09/30)
M25 F4	YCL043C	protein disulfide isomerase (57.45/62)
M22 A1	YCL044C	(45.90/46)
M265 F1	YCL045C	(83.63/85)
M148 D5	YCL049C	(34.45/64)
M148 D6	YCL050C	diadenosine 5' 5"-P1 P4-tetraphosphate phosphorylase I (35.34/50)

M148 E3	YCL055W	May assist Ste12p in pheromone-dependent expression of KAR3 and CIK1 (36.96/45)
M149 H7	YCL059C	Protein essential for cell division and spore germination (34.79/36)
M149 C1	YCL060C	(34.90/34)
M148 A3	YCL062W	(21.56/36)
M148 F3	YCL063W	(14.29/20)
M22 E3	YCL064C	catabolic serine (threonine) dehydratase (39.63/40)
M148 G7	YCL067C	(23.13/36)
M148 B1	YCL068C	(20.93/33)
M22 C4	YCL073C	(67.68/56)
M149 H4	YCL074W	(33.99/40)
M21 H2	YCL075W	(16.27/20)
M148 G6	YCLX01 W	(14.63/30)
M22 A5	YCLX03C	(14.00/18)
M148 H6	YCLX09 W	(14.41/36)
M148 A4	YCR002C	conserved potential GTP-binding protein (35.45/48)
M22 E6	YCR003W	Mitochondrial ribosomal protein MRPL32 (YmL32) (20.24/55)
M148 G5	YCR004C	(27.20/27)
M148 A7	YCR005C	non-mitochondrial citrate synthase (50.63/50)
M148 E1	YCR007C	(26.32/40)
M22 E7	YCR011C	ATP-dependent permease (115.42/?)
M148 H5	YCR012W	3-phosphoglycerate kinase (45.87/45)
M148 A6	YCR020C	(23.68/35)
M22 C9	YCR024C	(54.25/36)
M148 B5	YCR025C	(14.99/25)
M148 H1	YCR036W	ribokinase(36.74/50)
M148 D4	YCR039C	(23.13/33)
M148 C5	YCR040W	transcription factor involved in the regulation of the alpha-specific genes (19.46/33)

M21 F1	YCR045C	(54.04/57)
M149 E5	YCR047C	(30.38/40)
M151 C3	YCR054C	(61.96/61)
M151 B1	YCR060W	(12.32/16)
M151 D3	YCR062W	(13.31/30)
M151 G4	YCR063W	(17.48/17)
M26 H4	YCR065W	Dosage-dependent suppressor of cmd1-1 mutation\ shows homology to fork head family of DNA-binding proteins (58.63/60)
M151 G8	YCR066W	Zn finger protein putative ATPase (53.68/53)
M150 C1	YCR068W	(47.3/51)
M151 D6	YCR072C	(56.68/64)
M151 H8	YCR074C	(11.69/16)
M151 E2	YCR077C	Necessary for accurate chromosome transmission during cell division (87.70/98)
M26 A5	YCR082W	(14.29/16)
M151 A9	YCR083W	(14.08/17)
M150 F2	YCR086W	(21.01/36)
M150 C5	YCR088W	Actin binding protein (65.23/65)
M151 G7	YCR090C	(20.05/36)
M23 G5	YCR091W	Putative serine/threonine protein kinase most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily (79.97/80?)
M151 C5	YCR096C	(13.12/20)
M151 B9	YCR098C	(57.01/20)
M151 G2	YCR101C	(20.05/36)
M151 H3	YCR102C	(40.51/50)
M151 C9	YCR106W	(91.63/33)
M151 A4	YCRX03C	(11.25/16)
M150 C9	YCRX07W	(20.45/30)
M150 H6	YCRX13W	multicopy suppressor of los1-1 (34.76/50)
M26 C5	YCRX14W	(11.66/14)
M150 E10	YCRX16C	(16.86/28)

M26 F1	YCRX17W	(13.64/20)
M151 G5	YCRX20C	(11.46/64)
M150 E9	YDL002C	HMG1-box containing protein (22.46/36)
M151 D4	YDL006W	serine-threonine protein phosphatase (31.02/36)
M324 D1	YDL008W	(18.36/34)
M150 F9	YDL010W	(25.52/34)
M151 B2	YDL012C	132-410(11.88/18)
M150 F4	YDL014W	nucleolar protein homologous to mammalian fibrillarin (36.08/40)
M151 E8	YDL017W	protein kinase required for initiation of mitotic DNA synthesis (55.88/64)
M152 A1	YDL020C	Suppressor of sec63 (58.44/68)
M153 B2	YDL021W	(34.32/40)
M152 D3	YDL022W	glycerol-3-phosphate dehydrogenase (43.12/45)
M152 F2	YDL029W	146-1299 actin-related protein (43.12/45)
M152 E3	YDL030W	RNA splicing factor (58.41/64)
M153 E4	YDL031W	(109.56/109)
M153 H6	YDL033C	(45.90/55)
M153 H5	YDL040C	N-terminal acetyltransferase (93.97/36)
M152 E8	YDL042C	regulator of silent mating loci (61.85/68)
M152 D1	YDL044C	Necessary for the stability and/or processing of some large mitochondrial transcripts(48.43/55)
M153 D2	YDL045C	FAD synthetase (33.69/50)
M152 C6	YDL048C	(55.58/60)
M153 B7	YDL049C	KRE9 homolog (29.51/50)
M152 A10	YDL051W	Protein homologous to human La (SS-B) autoantigen (30.46/40)

M152 E1	YDL052C	putative 1-acyl-sn-glycerol-3-phosphate acyl transferase (33.46/40)
M152 B5	YDL055C	NDP-hexose pyrophosphorylase (39.74/45)
M27 E5	YDL056W	transcription factor (91.74/90)
M274 B2	YDL059C	(26.21/36)
M153 H4	YDL063C	(68.23/60)
M153 B6	YDL064W	149-584(17.48/20)
M153 D7	YDL065C	(38.53/38)
M152 G8	YDL066W	Mitochondrial form of NADP-specific isocitrate dehydrogenase (47.29/50)
M153 F2	YDL069C	translational activator of cytochrome b (25.66/36)
M153 G3	YDL070W	(70.39/70)
M28 E2	YDL072C	(22.46/30)
M153 C10	YDL075W	479-763(12.54/20)
M152 D5	YDL079C	705-1798 MDS1 related protein kinase (55.22/55)
M152 F7	YDL081C	ribosomal protein large subunit L12\ also known as L12eIIA (11.69/18)
M152 A2	YDL084W	(49.27/50)
M28 E1	YDL085W	(60.06/60)
M153 A4	YDL086W	(30.14/33)
M152 E5	YDL087C	EXit from Mitosis (28.74/38)
M27 F9	YDL089W	(53.45/45)
M333 C2	YDL090C	component of protein prenyltransferase (47.44/55)
M153 E10	YDL091C	(50.08/50)
M27 A10	YDL092W	Signal recognition particle subunit (16.27/16)
M152 B3	YDL093W	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase (81.84/82)
M153 B4	YDL094C	(18.62/40)
M255 H1	YDL097C	(47.77/54)
M152 C9	YDL098C	(21.47/32)
M333 D2	YDL099W	(37.62/42)
M152 C2	YDL100C	(38.97/45)
M152 C3	YDL101C	protein kinase (56.46/60)
M153 E5	YDL103C	(52.50/60)
M153 F6	YDL104C	(44.80/50)
M153 A8	YDL105W	(44.43/44)
M202 A2	YDL106C	Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes (61.52/100)
M153 G10	YDL107W	cox1 pre-mRNA splicing factor (38.72/40)
M152 D2	YDL108W	110-1002 serine-threonine kinase (33.77/40)
M152 E4	YDL110C	(16.53/32)
M29 E1	YDL120W	Mitochondrial protein that regulates mitochondrial iron accumulation iron accumulation (19.35/19)
M155 C6	YDL121C	(16.42/33)
M155 F8	YDL123W	(15.51/19)
M155 B1	YDL124W	(34.43/40)
M30 D2	YDL125C	209-588(17.49/28)
M29 C2	YDL126C	Microsomal protein of CDC48VPAS1VSEC1 8 family of ATPases\ full length homology to mammalian protein VCP\ involved in secretion peroxisome formation and gene expression (91.88/92)
M155 D6	YDL129W	(32.12/32)
M29 H2	YDL131W	(48.51/48)
M29 A3	YDL132W	Cell division cycle blocked at 36 degree C (89.76/90)
M29 C3	YDL134C	serine-threonine protein phosphatase 2A (40.62/40)
M29 G3	YDL137W	ADP-ribosylation factor 2 (20.02/20)
M29 H3	YDL138W	(84.04/84)

M155 D1	YDL139C	(27.20/37)
M29 C4	YDL141W	Biotin:apoprotein ligase (76.01/76)
M274 C2	YDL142C	Phosphatidylglycerophosphate Synthase (31.26/48)
M29 F4	YDL144C	(39.52/40)
M155 F7	YDL145C	(132.14/98)
M29 H4	YDL146W	(54.12/54)
M29 D5	YDL150W	RNA polymerase III (C) subunit (46.53/46)
M155 G7	YDL153C	Something About Silencing 10 (67.13/70)
M29 H5	YDL154W	(99.22/99)
M30 D1	YDL155W	G(sub)2-specific B-type cyclin (47.08/40)
M29 C6	YDL157C	(13.01/13)
M29 E6	YDL159W	MEK homolog (56.76/56)
M29 F6	YDL160C	(55.69/55)
M30 C4	YDL165W	(21.12/32)
M155 F4	YDL166C	(21.70/36)
M155 G6	YDL168W	Long-chain alcohol dehydrogenase (glytathione-dependent formaldehyde dehydrogenase) (42.57/32)
M29 H7	YDL170W	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type (58.29/58)
M155 G4	YDL174C	mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase (64.60/98)
M29 E8	YDL175C	(37.87/38)
M155 A8	YDL177C	(18.73/29)
M155 C9	YDL178W	D-Lactate Dehydrogenase (Cytochrome) (58.41/64)
M29 D9	YDL182W	(47.29/47)
M29 E9	YDL183C	(35.23/35)

M29 F9	YDL184C	Ribosomal protein RPL47 (YL41) (RPL47A and RPL47B code for identical proteins)(2.786/5)
M154 G1	YDL187C	(12.02/27)
M29 E10	YDL191W	495-854 Ribosomal protein (rat L35) (13.41/31)
M255 D2	YDL194W	glucose transporter (97.45/150)
M30 G4	YDL197C	Anti-silencing protein that causes depression of silent loci when overexpressed (57.78/60)
M29 D11	YDL198C	(33.03/33)
M29 E11	YDL199C	(75.60/75)
M310 G1	YDL200C	6-O-methylguanine-DNA methylase (22.69/34)
M155 D8	YDL201W	(31.57/42)
M30 B11	YDL202W	(27.5/27)
M155 B3	YDL204W	(43.34/54)
M29 C12	YDL205C	phorphobilinogen deaminase (uroporphyrinogen synthase) the third step in heme biosynthesis (36.00/36)
M154 C5	YDL206W	(83.93/115)
M155 C7	YDL208W	HMG-like nuclear protein (19.14/30)
M31 A1	YDL211C	(40.95/41)
M31 C1	YDL213C	(24.78/25)
M156 B3	YDL214C	(76.92/98)
M156 G4	YDL216C	(50.08/64)
M156 G6	YDL218W	(34.98/34)
M32 E2	YDL221W	(20.24/28)
M31 D2	YDL222C	(34.02/34)
M31 F2	YDL224C	(71.42/70)
M156 H5	YDL225W	(60.72/90)
M31 H2	YDL226C	ADP-ribosylation factor GTPase-activating protein (ARF GAP) (38.75/38)
M31 F3	YDL232W	3.6-kDa protein probably membrane-located (4.07/4)

M157 B8	YDL234C	(82.09/98)
M157 D1	YDL235C	Two-component phosphorelay intermediate (18.40/28)
M156 F1	YDL236W	p-nitrophenyl phosphatase (34.43/40)
M157 E3	YDL237W	(43.01/50)
M31 G4	YDL241W	(13.64/13)
M156 B7	YDL242W	(12.98/18)
M156 G1	YDL244W	(37.51/52)
M156 D3	YDL246C	(39.30/53)
M156 B5	YDL248W	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p Ybr302p Cos3p Cos1p Cos4p Cos8p Cos6p Cos9p (42.24/48)
M156 B6	YDR001C	(82.64/60)
M31 H5	YDR002W	(22.22/22)
M32 C1	YDR003W	(23.21/38)
M31 C6	YDR005C	87-1268(43.56/46)
M31 D6	YDR006C	(99.14/99)
M31 F6	YDR008C	(12.79/13)
M31 G6	YDR009W	galactokinase(57.31/57)
M32 A2	YDR012W	large ribosomal subunit protein L2B\ highly similar to ribosomal protein L2A (Rpl2bp) (39.93/45)
M31 F7	YDR016C	(10.47/10)
M31 A8	YDR019C	glycine cleavage T protein (T subunit of glycine decarboxylase complex (44.03/44)
M31 B8	YDR020C	(25.55/25)
M156 G2	YDR021W	(44/48)
M31 D8	YDR022C	cik1 suppressor (21./5922)
M156 C4	YDR023W	seryl-tRNA synthetase (50.9/350)
M31 F8	YDR024W	(17.82/18)
M31 G8	YDR025W	385-810 ribosomal protein S18 (17.27/20)

M156 G3	YDR030C	Protein involved in the same pathway as Rad26p has beta-transducin (WD-40) repeats (55.69/55)
M156 D4	YDR031W	(12.98/18)
M31 F9	YDR032C	(21.81/30)
M157 H1	YDR035W	DAHP synthase\ a.k.a. phospho-2-dehydro-3-deoxyheptonate aldolase phenylalanine-inhibited\ phospho-2-keto-3-deoxyheptonate aldolase\ 2-dehydro-3-deoxyphosphoheptonate aldolase\ 3-deoxy-D-arabine-heptulosonate-7-phosphate synthase (40.81/48)
M156 B2	YDR036C	(55.03/55)
M32 B3	YDR037W	lysyl-tRNA synthetase (65.12/55)
M156 E7	YDR042C	(22.03/28)
M31 A11	YDR043C	(25.44/25)
M156 C2	YDR044W	Coproporphyrinogen III oxidase (36.29/44)
M32 C5	YDR047W	(39.93/45)
M31 F11	YDR048C	(11.47/12)
M31 G11	YDR049W	(69.63/769)
M156 F7	YDR050C	triosephosphate isomerase (27.31/33)
M32 G1	YDR051C	(36.77/40)
M32 D3	YDR053W	(14.52/16)
M32 F4	YDR054C	ubiquitin-conjugating enzyme E2 (32.48/50)
M31 F12	YDR056C	(22.58/21)
M34 D2	YDR060W	(112.86/112)
M33 C1	YDR061W	(59.4/60)
M159 A5	YDR063W	(16.5/30)
M158 G6	YDR066C	(21.59/33)
M158 B1	YDR067C	(24.67/35)
M34 C4	YDR070C	(10.36/12)
M159 B5	YDR071C	(21.04/30)
M34 B1	YDR075W	protein phosphatase type 2A (33.99/40)
M34 C1	YDR083W	(44.33/41)
M255 G2	YDR087C	(30.61/48)

M158 A5	YDR088C	involved in 3' splice site choices (42.05/52)
M158 C2	YDR092W	299-730 ubiquitin-conjugating enzyme (16.94/30)
M301 F1	YDR097C	(136.65/140)
M158 C6	YDR113C	42-kDa nuclear protein (41.06/55)
M34 E7	YDR114C	(11.03/16)
M159 F3	YDR117C	(62.28/64)
M33 G8	YDR121W	(21.67/40)
M33 H10	YDR138W	(82.83/80)
M34 C2	YDR147W	(58.85/45)
M159 B6	YDR151C	(35.78/48)
M158 F6	YDR153C	(45.24/60)
M35 A1	YDR155C	cyclophilin peptidyl-prolyl cis-trans isomerase (17.85/18)
M160 B2	YDR156W	RNA polymerase I subunit A14 (15.28/25)
M36 A4	YDR158W	aspartic beta semi-aldehyde dehydrogenase (40.36/45)
M161 C6	YDR161W	PTC1-Interacting Protein (42.68/50)
M36 A8	YDR162C	(25.99/36)
M160 B1	YDR163W	(19.46/32)
M160 D4	YDR167W	TFIID subunit (22.77/34)
M160 D5	YDR168W	(55.77/60)
M160 E6	YDR169C	sin3 binding protein (56.46/66)
M160 C1	YDR171W	Similar to HSP26\ expression is regulated by stress conditions (41.46/50)
M35 C3	YDR173C	(39.08/?)
M160 F3	YDR174W	(27.27/28)
M161 C4	YDR175C	(35.12/45)
M36 E7	YDR177W	ubiquitin-conjugating enzyme (23.76/34)
M161 D1	YDR179C	(17.85/31)
M36 E6	YDR183W	(25.41/36)
M160 G6	YDR184C	(32.47/45)
M35 A5	YDR186C	(96.50/?)

M160 H2	YDR188W	Cytoplasmic chaperonin of the Cct ring complex (previously called TCP1 or TRiC) distantly related to Tcp1p and to Hsp60 (60.27/64)
M35 D5	YDR189W	(73.47/75)
M161 D4	YDR190C	(50.96/55)
M161 E5	YDR191W	(40.81/50)
M36 F7	YDR192C	nucleoporin(47.33/53)
M35 A6	YDR194C	Mitochondrial RNA helicase of the DEAD box family (73.07/?)
M35 B6	YDR195W	(58.74/60)
M161 B3	YDR196C	(26.54/33)
M35 D6	YDR197W	cytochrome b translational activator (42.9/?)
M161 E4	YDR198C	(52.72/34)
M160 G7	YDR201W	(18.36/34)
M160 F1	YDR202C	(38.64/45)
M161 C3	YDR204W	responsible for restoring ubiquinone biosynthesis in coq4 mutant (36.96/45)
M161 F1	YDR210W	(8.46/16)
M35 D8	YDR213W	(100.5/4?)
M160 A5	YDR214W	(38.61/50)
M36 G3	YDR220C	(10.70/14)
M160 B6	YDR223W	(51.48/66)
M160 B7	YDR224C	Histone H2B (HTB1 and HTB2 code for nearly identical proteins) (14.44/18)
M160 A8	YDR225W	Histone H2A (HTA1 and HTA2 code for nearly identical proteins) (14.63/18)
M35 A10	YDR226W	cytosolic adenylate kinase (24.53/25)
M35 B10	YDR227W	regulator of silent mating loci (149.49/?)
M160 C4	YDR229W	(49.94/55)
M35 H12	YDR249C	(41.06/?)
M38 H1	YDR251W	(91.41/98)

M162 E2	YDR252W	Negative effect on expression of several genes transcribed by RNA polymerase II\ BTF3 homolog (16.5/20)
M37 D1	YDR253C	zinc finger DNA binding factor transcriptional regulator of sulfur amino acid metabolism (21.04/?)
M163 G6	YDR255C	(46.34/60)
M37 G1	YDR256C	catalase A (56.68/60)
M163 C9	YDR257C	(54.47/64)
M163 D2	YDR259C	(42.26/60)
M162 D4	YDR262W	(30.03/36)
M37 F2	YDR263C	DNA-damage inducible gene (47.33/?)
M162 A6	YDR264C	(84.07/55)
M163 B1	YDR266C	(70.32/80)
M163 E3	YDR268W	mitochondrial tryptophanyl-tRNA synthetase (41.8/49)
M37 F3	YDR271C	(13.56/14)
M163 C8	YDR272W	Cytoplasmic glyoxylase-II (30.35/40)
M38 E8	YDR273W	(40.36/50)
M162 B2	YDR275W	(25.96/38)
M163 F3	YDR276C	(6.086/6)
M37 F4	YDR279W	(38.61/38)
M163 D1	YDR282C	(45.57/55)
M162 H2	YDR284C	Diacylglycerol Pyrophosphate Phosphatase (31.82/38)
M38 E6	YDR287W	(32.12/38)
M163 G9	YDR289C	(45.02/64)
M38 D1	YDR290W	(12.1/15)
M38 C4	YDR293C	putative protein phosphatase (137.5/3130)
M37 E6	YDR294C	(64.82/?)
M163 F1	YDR298C	ATP synthase subunit 5\ oligomycin sensitivity-conferring protein (23.45/30)
M163 A4	YDR300C	gamma-glutamyl kinase (47.11/48)
M37 F7	YDR303C	(97.48/?)

M37 G7	YDR304C	Cyclophilin D Peptidyl-prolyl cis-trans isomerase D (24.86/40)
M163 A10	YDR305C	177-743 Yeast member of the Histidine Triad protein family (HIT) (27.27/35)
M163 G2	YDR307W	(72.93/75)
M163 B4	YDR308C	RNA polymerase II holoenzyme component (15.43/31)
M38 E4	YDR309C	(42.26/48)
M163 H1	YDR314C	(76.25/85)
M163 H2	YDR315C	(30.94/40)
M163 G8	YDR320C	(73.51/110)
M163 C10	YDR321W	Asparaginase I intracellular isozyme (42.02/50)
M163 D4	YDR324C	(85.49/95)
M163 A2	YDR330W	(55.11/70)
M163 A3	YDR331W	Protein involved in the attachment of glycosylphosphatidylinositol (GPI) anchors to proteins(45.32/62)
M163 A9	YDR336W	(34.65/45)
M163 E10	YDR337W	Mitochondrial ribosomal protein MRPS28 (E. coli S15) (31.57/40)
M163 B2	YDR338C	(76.48/76)
M163 B3	YDR339C	(20.82/33)
M163 E5	YDR341C	(66.80/70)
M170 A1	YDR346C	(52.94/60)
M170 C9	YDR353W	Thioredoxin reductase (35.2/48)
M170 B1	YDR354W	anthranilate phosphoribosyl transferase (41.91/50)
M274 C3	YDR354W	anthranilate phosphoribosyl transferase (41.91/45)
M171 F2	YDR356W	putative nucleoskeleton component (103.95/120)
M171 F3	YDR357C	(13.45/20)
M170 D2	YDR363W	(50.37/55)
M171 B2	YDR363W	(50.37/54)
M171 G3	YDR365C	(69.11/72)

M171 H5	YDR367W	132-767(24.42/38)
M274 E3	YDR369C	DNA repair protein (93.97/98)
M39 A4	YDR370C	(48.65/45)
M171 H3	YDR373W	(21.01/32)
M171 C7	YDR376W	adrenodoxin oxidoreductase homolog (54.34/64)
M171 E8	YDR377W	ATP synthase subunit f (11.22/20)
M171 D1	YDR378C	(13.56/20)
M171 A4	YDR381W	Nuclear RNA-binding RNA annealing protein (11.77/18)
M40 B6	YDR383C	(27.75/34)
M40 H7	YDR385W	translation elongation factor 2 (EF-2) (92.73/85)
M39 A6	YDR386W	(69.63/70)
M39 D6	YDR389W	GTPase activating protein (GAP) for RHO1 (72.05/72)
M171 E1	YDR394W	(47.29/50)
M171 C4	YDR397C	130-533(16.27/30)
M171 C5	YDR398W	(70.84/70)
M171 C6	YDR399W	(24.42/34)
M171 F7	YDR400W	(41.69/50)
M171 G7	YDR408C	glycinamide ribotide transformylase (23.57/33)
M171 C3	YDR412W	(25.96/50)
M171 D6	YDR415C	(41.27/50)
M171 E6	YDR423C	(45.02/51)
M171 D3	YDR428C	(28.74/38)
M171 E4	YDR429C	(30.27/40)
M171 E5	YDR430C	(108.82/120)
M170 A9	YDR432W	RNA binding protein involved in mitochondrial protein targeting (45.65/48)
M171 H1	YDR434W	(58.85/98)
M171 E2	YDR435C	(36.11/46)
M171 E3	YDR436W	serine-threonine phosphatase Z (78.21/88)
M171 G6	YDR439W	(38.38/52)
M41 C1	YDR444W	(75.68/100)
M173 B6	YDR446W	ExtraCellular Mutant (33.33/42)

M41 F1	YDR447C	318-725 Ribosomal protein RP51B (rat S17) (15.07/26)
M42 B8	YDR448W	(47.85/55)
M41 A2	YDR450W	483-876(16.27/20)
M173 E3	YDR452W	(74.35/98)
M41 D2	YDR453C	(21.59/21)
M173 C6	YDR454C	guanylate kinase (20.60/31)
M173 G3	YDR468C	(24.67/38)
M42 C7	YDR471W	416-795 60S ribosomal protein L27 identical to Yhr010p (15.07/28)
M42 H9	YDR473C	(51.62/55)
M42 E1	YDR474C	(61.08/60)
M173 H3	YDR476C	(24.67/33)
M172 D6	YDR478W	interstrand crosslink repair protein (21.89/36)
M173 H7	YDR479C	(60.97/64)
M172 A9	YDR480W	MAP kinase-associated protein (35.64/52)
M173 F10	YDR481C	repressible alkaline phosphatase (62.39/70)
M172 B1	YDR482C	(14.88/28)
M173 C5	YDR485C	(89.13/89)
M173 G6	YDR486C	(28.85/38)
M172 G7	YDR487C	3 4-dihydroxy-2-butanone 4-phosphate synthase (22.91/34)
M42 G8	YDR488C	(58.66/48)
M173 G10	YDR489W	(32.45/36)
M173 D5	YDR493W	(13.64/23)
M173 E1	YDR498C	membrane glycoprotein sorted by HDEL retrieval system (42.26/60)
M173 H2	YDR499W	(82.38/92)
M173 A7	YDR502C	S-adenosylmethionine synthetase (42.37/33)
M41 E9	YDR510W	Suppressor of Mif Two (11.22/20)
M173 G9	YDR512C	(20.60/28)
M172 F10	YDR513W	Glutaredoxin (thioltransferase) (glutathione reductase) (15.84/28)

M173 A3	YDR515W	regulates the copper-dependent mineralization of copper sulfide complexes on the cell surface in cells cultured in medium containing copper salts (49.38/50)
M173 C4	YDR516C	(55.03/64)
M172 E5	YDR517W	(41.03/55)
M173 C7	YDR518W	Protein disulfide isomerase homolog (56.98/56)
M173 E8	YDR519W	FKBP (FK506 binding protein) 13\ peptidylprolyl cis-trans isomerase activity (14.96/16)
M173 D4	YDR524C	(53.05/60)
M173 F8	YDR527W	(48.4/48)
M172 H1	YDR530C	5' 5"-P-1 P-4-tetraphosphate phosphorylase II (35.78/50)
M173 C3	YDR531W	(40.48/50)
M173 A6	YDR533C	(26.10/26)
M42 G6	YDR534C	(58.11/58)
M174 E3	YDR540C	(19.72/34)
M175 G3	YEL003W	Polypeptide 2 of a Yeast Non-native Actin Binding Complex homolog of a component of the bovine NABC complex (13.64/30)
M175 B5	YEL004W	(37.73/42)
M175 A9	YEL007W	(73.47/97)
M174 C1	YEL009C	transcriptional activator of amino acid biosynthetic genes (30.94/55)
M175 C5	YEL012W	ubiquitin-conjugating enzyme\ ubiquitin-protein ligase (22.77/36)
M3 G7	YEL015W	(60.72/64)
M175 C10	YEL016C	(54.36/90)
M175 F2	YEL017W	(37.28/47)
M175 A4	YEL018W	(30.8/38)

M175 D5	YEL019C	Protein involved in DNA repair (29.40/36)
M3 G6	YEL021W	orotidine-5'-phosphate decarboxylase (29.48/35)
M3 D1	YEL024W	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex (23.76/30)
M175 B4	YEL026W	(13.97/16)
M175 A8	YEL029C	(34.45/47)
M174 H8	YEL030W	ExtraCellular Mutant (70.95/98)
M310 C2	YEL034W	Translation initiation factor eIF-5A (17.48/30)
M174 E5	YEL035C	(18.39/28)
M174 G6	YEL036C	Mannan 8\ Protein of the endoplasmic reticulum with a role in retention of glycosyltransferases in the Golgi also involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol (55.03/55)
M174 H7	YEL037C	ubiquitin-like protein (43.81/60)
M175 F10	YEL039C	iso-2-cytochrome c (12.46/22)
M3 A3	YEL041W	(54.56/60)
M3 C6	YEL044W	(18.47/20)
M3 C8	YEL046C	Threonine Aldolase (42.60/50)
M175 G1	YEL048C	(16.75/26)
M3 B3	YEL049W	member of the seripauperin protein\gene family (see Gene_class PAU) (13.31/15)
M174 G5	YEL051W	Vacuolar H-ATPase D subunit of the V1 catalytic sector (28.37/40)
M3 D6	YEL052W	ATPase family gene (56.1/60)

M175 H1	YEL056W	subunit of a cytoplasmic histone acetyltransferase (44.22/54)	M176 A6	YER058W	Required for assembly of active cytochrome c oxidase (11.88/16)
M3 C4	YEL058W	Phosphoacetylglucosamine Mutase (61.38/64)	M176 D3	YER062C	DL-glycerol-3-phosphatase(27.53/36)
M3 E8	YEL061C	(114.21/114)	M177 H3	YER063W	(24.09/50)
M3 D9	YEL062W	Non-membrane-embedded PEST sequence-containing protein (68.75/68)	M5 A6	YER069W	N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase (95.04/100)
M174 A2	YEL063C	arginine permease (64.93/55)	M176 F2	YER076C	(33.35/50)
M3 C3	YEL064C	(52.83/36)	M5 B6	YER077C	(75.71/80)
M174 H5	YEL066W	(19.8/32)	M177 B5	YER079W	(23.21/36)
M3 E9	YEL070W	(55.33/60)	M5 C2	YER089C	Protein phosphatase type 2C (51.07/55)
M3 B2	YEL071W	(54.67/55)	M178 C4	YER101C	(47.33/60)
M3 D3	YEL072W	(25.52/32)	M179 B6	YER102W	(22.11/36)
M175 H4	YEL073C	(11.80/26)	M179 B7	YER103W	member of 70 kDa heat shock protein family (70.73/98)
M3 E3	YER001W	Alpha-1 3-mannosyltransferase (83.93/83)	M179 A1	YER104W	(22.99/38)
M174 H4	YER002W	(25.52/38)	M178 D4	YER109C	putative transcriptional activator of FLO1 (15.54/28)
M175 F7	YER004W	(25.52/34)	M7 A3	YER112W	U6 snRNA-associated protein (20.68/55)
M310 D2	YER005W	(69.41/79)	M179 C6	YER118C	Transmembrane osmosensor (40.40/50)
M174 D9	YER006W	(57.31/64)	M178 B6	YER119C	(49.31/49)
M177 F2	YER010C	(25.77/40)	M178 D5	YER125W	Suppressor of mutations in SPT3 (89.1/89)
M177 C6	YER014W	protoporphyrinogen oxidase (59.4/64)	M178 D1	YER127W	(39.48/50)
M265 B3	YER015W	Acyl-CoA synthetase (fatty acid activator 2) (81.95/91)	M255 C3	YER128W	(22.44/37)
M176 E1	YER016W	(37.95/50)	M8 D3	YER130C	(48.76/55)
M5 E8	YER020W	nucleotide binding regulatory protein (49.5/42)	M8 D4	YER131W	(13.2/20)
M176 F1	YER023W	delta 1-pyrroline-5-carboxylate reductase (31.57/38)	M178 H1	YER136W	GDP dissociation inhibitor (49.72/98)
M176 F6	YER029C	(21.59/34)	M178 C2	YER137C	(16.31/29)
M177 A1	YER030W	(17.71/42)	M202 A3	YER150W	(16.49/60)
M176 H3	YER034W	(20.46/36)	M179 C2	YER152C	(48.76/60)
M176 G6	YER037W	(35.42/48)	M178 D2	YER153C	translational activator of cytochrome c oxidase subunit III (27.97/35)
M177 F3	YER042W	(20.45/32)	M178 E3	YER154W	(44.33/50)
M176 C3	YER048C	DnaJ homolog with a leucine zipper (43.04/52)	M178 G4	YER156C	(37.21/45)
M176 D2	YER055C	ATP phosphoribosyltransferase (32.70/36)			

M178 E1	YER159C	transcription factor (15.65/30)
M178 E2	YER161C	non-specific DNA binding protein (sin1) (36.66/50)
M178 G5	YER165W	Poly(A) binding protein cytoplasmic and nuclear (63.58/98)
M178 F3	YER170W	Adenylate kinase (mitochondrial GTP:AMP phosphotransferase) (24.86/33)
M9 F3	YFL-TYA	(/75)
M267 A1	YFL001W	Similar to rRNA methyltransferase (Caenorhabditis elegans) and hypothetical 28K protein (alkaline endoglucanase gene 5' region) from Bacillus sp. (4/8.7353)
M267 E2	YFL002C	ATP-dependent RNA helicase (66./6966)
M275 B5	YFL005W	Ras-like small GTP-binding protein (23.7/633)
M275 E6	YFL006W	(28.05/35)
M267 F2	YFL010C	(23.24/34)
M267 C6	YFL012W	(16.49/23)
M275 F6	YFL013C	(76.25/89)
M267 G2	YFL016C	DnaJ homolog involved in mitochondrial biogenesis and protein folding (56.24/56)
M10 C3	YFL017C	(17.52/?)
M275 C4	YFL018C	dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes) (54.92/54)

M9 A10	YFL021W	transcriptional activator with GATA-1-type Zn finger DNA-binding motif (56.21/40)
M267 D1	YFL022C	Phenylalanyl-tRNA synthetase beta subunit cytoplasmic (55.46/59)
M267 H2	YFL023W	(87.67/105)
M267 A4	YFL024C	(91.55/101)
M267 F7	YFL027C	(54.70/60)
M267 G8	YFL028C	ABC ATPase (31.82/34)
M267 H9	YFL029C	Cyclin-dependent kinase-activating kinase (40.51/50)
M267 G7	YFL035C	Mob1p-like protein (28.52/37)
M10 B6	YFL037W	beta-tubulin(50.48/?)
M9 E4	YFL038C	Ras-like GTP-binding protein\ most similar to mammalian Rab1A protein (22.69/30)
M274 G3	YFL039C	319-1436 Actin (41.46/49)
M275 F5	YFL040W	(59.51/50)
M275 A7	YFL041W	(68.53/98)
M275 A9	YFL043C	(15.98/27)
M9 G1	YFL044C	(33.14/40)
M9 C3	YFL045C	phosphomannomutase (27.97/35)
M9 F4	YFL046W	(22.88/32)
M10 D7	YFL047W	(78.65/98)
M267 F6	YFL048C	47 kDa type I transmembrane protein localized to the Golgi (48.98/55)
M267 A9	YFL050C	ALuminium Resistance 2 (94.41/104)
M275 B9	YFL051C	(17.63/34)
M275 G1	YFL052W	(51.36/49)
M255 D3	YFL053W	(65.12/98)
M275 H3	YFL054C	(71.09/65)
M275 H5	YFL056C	(23.45/32)
M275 B7	YFL057C	(16.75/25)
M267 B9	YFL058W	a thiamine regulated pyrimidine precursor biosynthesis enzyme (37.51/42)
M275 C9	YFL059W	(32.89/47)

M275 H1	YFL060C	SNZ3 proximal ORF stationary phase induced gene family (24.45/33)
M275 B3	YFL061W	(24.86/32)
M275 A4	YFL062W	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p Ybr302p Cos3p Cos1p Cos4p Cos8p Cos6p Cos9p (41.8/48)
M9 B2	YFL068W	(17.71/25)
M267 G5	YFR001W	(22.55/32)
M255 E3	YFR003C	(17.08/41)
M275 C8	YFR004W	Similar to <i>S. pombe</i> PAD1 gene product (33.77/46)
M275 D9	YFR005C	(49.31/56)
M10 A11	YFR006W	(58.96/?)
M9 G3	YFR007W	(38.94/45)
M267 G4	YFR008W	(24.42/36)
M275 H4	YFR009W	Member of ATP-binding cassette (ABC) family of proteins (82.83/80)
M10 E11	YFR010W	(55/55)
M267 E8	YFR011C	(18.7/320)
M275 D8	YFR012W	(22.33/27)
M275 E9	YFR013W	(86.68/170)
M9 D2	YFR014C	calmodulin dependent protein kinase (49.09/40)
M202 C3	YFR015C	Glycogen synthase (UDP-glucose--starch glucosyltransferase) (77.91/110)
M275 A5	YFR017C	(21.48/35)
M267 C7	YFR018C	(39.96/52)
M275 F9	YFR021W	(55.11/96)
M272 A1	YFR022W	(80.74/101)
M272 E2	YFR023W	poly(A) binding protein\ related to PES4 protein homolog YHR015w (67.32/70)
M273 A4	YFR024C	(41.06/50)
M43 A6	YFR025C	Histidinolphosphatase (36.88/45)
M273 B8	YFR026C	(18.62/34)

M272 D10	YFR028C	soluble tyrosine-specific protein phosphatase (60.64/62)
M43 B6	YFR032C	(31.82/34)
M272 H7	YFR033C	ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa) (16.20/26)
M43 C8	YFR034C	myc-type helix-loop-helix transcription factor (34.45/48)
M272 G2	YFR037C	(61.30/70)
M272 B5	YFR039C	(56.13/64)
M43 C6	YFR040W	155 kDa SIT4 protein phosphatase-associated protein (99.66/100)
M273 H6	YFR040W	155 kDa SIT4 protein phosphatase-associated protein (99.66/99)
M272 A8	YFR041C	(32.48/40)
M272 F10	YFR043C	(26.10/33)
M272 D1	YFR044C	(52.94/54)
M255 G3	YFR045W	(19.69/50)
M272 C4	YFR046C	(39.74/52)
M43 B5	YFR047C	(32.48/40)
M255 B4	YFR048W	(72.93/81)
M333 C3	YFR049W	mitochondrial ribosomal protein (precursor) (13.64/14)
M255 C4	YFR050C	proteasome subunit necessary for peptidyl glutamyl peptide hydrolyzing activity (29.39/40)
M273 E1	YFR052W	cytoplasmic 32 - 34 kDa protein (30.35/55)
M272 A3	YFR053C	Hexokinase I (PI) (also called Hexokinase A) (53.48/55)
M273 G5	YFR055W	(37.51/45)
M274 A4	YGL001C	(38.42/49)
M272 H10	YGL002W	(23.87/29)
M273 F1	YGL003C	(62.39/63)
M273 B3	YGL004C	(45.90/52)
M272 E4	YGL005C	(30.72/40)

M272 D8	YGL008C	plasma membrane H ⁺ -ATPase (101.01/105)	M43 C10	YGL050W	(30.14/35)
M272 F9	YGL009C	isopropylmalate isomerase (85.72/95)	M301 A2	YGL052W	(11.22/18)
M273 G1	YGL011C	Proteasome subunit YC7alphaVY8 (protease yscE subunit 7) (27.75/31)	M272 A5	YGL053W	(26.28/36)
M273 C3	YGL012W	Sterol C-24 reductase (52.14/50)	M272 B6	YGL054C	(15.21/20)
M324 E2	YGL014W	(97.79/105)	M273 A8	YGL055W	delta-9-fatty acid desaturase (56.21/60)
M273 A10	YGL017W	arginyl-tRNA-protein transferase (55.44/70)	M43 A8	YGL056C	(58.00/60)
M272 A11	YGL018C	(20.37/30)	M272 C10	YGL057C	(31.60/34)
M272 H1	YGL019W	casein kinase II beta chain (30.69/40)	M202 E3	YGL058W	Ubiquitin conjugating enzyme involved in an error-prone DNA-damage recovery pathway (19.03/33)
M273 D3	YGL020C	(25.88/34)	M310 A3	YGL059W	(49.06/60)
M272 B7	YGL023C	(69.88/79)	M45 E1	YGL061C	(27.20/?)
M272 H9	YGL025C	Probable transcription factor polyglutamine domain protein (47.44/50)	M180 B1	YGL067W	(42.45/50)
M272 B11	YGL026C	tryptophan synthetase (77.80/82)	M180 A2	YGL068W	(21.45/32)
M273 A2	YGL027C	(91.66/104)	M180 C1	YGL075C	(42.60/50)
M273 E3	YGL028C	(59.65/64)	M181 E5	YGL080W	(14.41/33)
M272 F4	YGL029W	(13.31/22)	M181 G7	YGL082W	(42.02/62)
M273 B6	YGL030W	234-548 large ribosomal subunit protein 32 (11.66/32)	M181 B5	YGL087C	97-499 homolog of human CROC-1 gene protects yeast cells from DNA damage (15.28/25)
M272 C7	YGL031C	Ribosomal protein RPL30A (rp29) (YL21) (17.08/25)	M180 H8	YGL090W	(46.42/64)
M272 E8	YGL032C	adhesion subunit of a-agglutinin (9.606/20)	M181 G5	YGL096W	(30.47/20)
M43 B2	YGL035C	Zinc-finger protein (55.47/60)	M180 D3	YGL101W	(23.76/34)
M272 H5	YGL038C	membrane-bound mannosyltransferase (52.83/64)	M180 C4	YGL102C	(15.65/16)
M272 D7	YGL039W	(38.49/45)	M180 H7	YGL105W	associated with tRNA and amino acyl-tRNA synthetases. (41.47/52)
M272 C2	YGL043W	RNA polymerase II elongation factor (34.1/43)	M180 B9	YGL106W	myosin light chain (16.5/20)
M44 F3	YGL044C	(32.59/40)	M180 E1	YGL107C	(71.09/68)
M272 A6	YGL046W	(28.93/35)	M180 E2	YGL108C	(15.43/20)
M273 H7	YGL047W	(22.33/31)	M180 D5	YGL111W	(51.04/51)
M273 D10	YGL049C	mRNA cap-binding protein (eIF-4F) 130K subunit (100.57/101)	M180 A8	YGL113W	(73.59/54)
			M181 D1	YGL115W	Protein involved in derepression of glucose-repressed genes (35.53/48)
			M310 B3	YGL116W	beta-transducin homolog (67.21/70)
			M180 C9	YGL122C	nuclear polyadenylated RNA binding protein (57.78/64)
			M180 G1	YGL123W	ribosomal protein S4 (28.05/34)

M180 G3	YGL125W	methylenetetrahydrofolate reductase (mthfr) (66/66)
M181 D4	YGL126W	(41.9/141)
M45 A2	YGL134W	PHO85 cyclin (47.7/450)
M44 G7	YGL138C	(37.98/52)
M44 H7	YGL146C	(34.24/36)
M181 F1	YGL147C	Ribosomal protein YL11 (rp25) (rp24) (E. coli L6) (rat L9) (21.04/40)
M181 G2	YGL148W	Chorismate synthase (41.47/50)
M181 E7	YGL153W	Peroxisomal peripheral membrane protein (peroxin) (37.62/57)
M182 A1	YGL155W	polypeptide subunit of a yeast type I protein geranylgeranyltransferase (41.47/41)
M183 C3	YGL157W	(38.38/38)
M182 A2	YGL164C	(48.43/64)
M182 D4	YGL166W	regulator of metallothionein (CUP1) expression (24.86/36)
M183 A8	YGL169W	Protein involved in translation initiation (46.97/46)
M182 B1	YGL171W	Contains domains found in the DEAD protein family of ATP-dependent RNA helicases; high-copy suppressor of kem1 null mutant (62.25/64)
M183 B2	YGL172W	nuclear pore complex protein with GLFG repetitive sequence motif (52.03/60)
M182 E4	YGL174W	(29.47/36)
M182 G5	YGL175C	(37.98/55)
M183 B1	YGL179C	(61.63/77)
M183 E3	YGL181W	Glycine-threonine-serine repeat protein (43.67/54)
M182 A7	YGL184C	(51.28/51)
M183 C8	YGL185C	(41.72/48)

M183 H5	YGL191W	subunit VIa of cytochrome c oxidase (14.3/16)
M183 D8	YGL193C	(11.46/16)
M182 E9	YGL194C	Protein with similarity to Hda1p Rpd3p Hos1p and Hos3p (49.75/64)
M182 C7	YGL200C	type I transmembrane protein component of COPII-coated ER-derived transport vesicles (22.46/32)
M183 H3	YGL205W	fatty-acyl coenzyme A oxidase (82.49/82)
M183 B6	YGL207W	transcription factor (113.96/113)
M182 G9	YGL210W	ras-like GTPase (24.53/32)
M274 B4	YGL213C	antiviral protein (43.70/52)
M183 G7	YGL216W	(88.66/90)
M182 G2	YGL220W	(13.31/16)
M183 B4	YGL221C	(31.71/36)
M183 A5	YGL222C	(19.38/19)
M183 D6	YGL223C	(45.90/54)
M182 F7	YGL224C	(30.83/38)
M183 G9	YGL226W	(13.64/13)
M182 H2	YGL228W	(63.58/63)
M183 B5	YGL230C	(16.20/27)
M182 G7	YGL232W	116-928(31.9/38)
M182 B10	YGL234W	glycinamide ribotide synthetase and aminoimidazole ribotide synthetase (88.33/88)
M182 B4	YGL237C	transcriptional activator protein of CYC1 (29.28/36)
M182 H7	YGL240W	(31.24/38)
M182 C10	YGL242C	(19.94/32)
M182 H1	YGL243W	(44.11/50)
M183 B3	YGL244W	nuclear protein unknown function (61.49/68)
M183 D4	YGL245W	(79.75/79)
M183 G6	YGL247W	(21.78/30)
M182 D10	YGL250W	(27.06/38)

M256 D3	YGL253W	Hexokinase II (PII) (also called Hexokinase B) (53.57/55)
M256 E4	YGL254W	Sulfur permease II (33/36)
M184 G6	YGL256W	alcohol dehydrogenase isoenzyme IV (51.2651)
M46 A6	YGL258W	(22.7/723)
M184 A1	YGL259W	(18.36/28)
M256 G6	YGR001C	443-675(21.34/31)
M256 A8	YGR002C	(52.49/58)
M256 B9	YGR003W	(81.95/90)
M256 B1	YGR004W	(50.93/55)
M256 D2	YGR005C	transcription initiation factor TFIIF middle subunit (44.03/60)
M184 F4	YGR007W	choline phosphate cytidyltransferase (also called phosphoethanolamine cytidyltransferase or phosphocholine cytidyltransferase) (35.64/36)
M184 H5	YGR008C	(9.376/9)
M256 B8	YGR010W	(43.56/51)
M256 E2	YGR013W	(68.31/75)
M46 H2	YGR015C	(36.11/40)
M184 A6	YGR016W	(21.01/30)
M184 B7	YGR017W	(32.78/38)
M256 C8	YGR018C	(12.02/17)
M256 D9	YGR019W	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) (51.92/54)
M184 E2	YGR021W	(32.01/38)
M184 B6	YGR024C	(26.10/34)
M256 E9	YGR027C	(11.91/16)
M256 E1	YGR028W	40 kDa putative membrane-spanning ATPase (39.93/50)
M256 G2	YGR029W	(12.98/16)
M184 A5	YGR031W	(37.73/38)
M256 C7	YGR033C	(26.32/31)
M256 F9	YGR035C	(12.79/17)

M256 H2	YGR037C	Acyl-CoA-binding protein (ACBP)VDiazepam binding inhibitor (DBI)Vendozepine (EP) (9.606/14)
M184 A4	YGR038W	(24.53/34)
M184 B5	YGR039W	(11.44/11)
M184 C6	YGR040W	MAP protein kinase homolog involved in pheromone signal transduction (40.59/50)
M256 D7	YGR041W	(60.38/63)
M184 F8	YGR042W	(29.92/32)
M256 G9	YGR043C	(36.66/44)
M184 F1	YGR044C	negative regulator of meiosis (33.03/36)
M256 C5	YGR047C	transcription factor tau (TFIIC) subunit 131 (112.78/115)
M184 D6	YGR048W	(39.82/50)
M256 E7	YGR049W	Protein that suppresses ts allele of CDC4 when overexpressed (20.68/30)
M184 A10	YGR051C	(11.80/12)
M184 G1	YGR068C	(64.49/48)
M46 A4	YGR072W	up-frameshift suppressor (42.68/45)
M256 G8	YGR074W	Homolog of human core snRNP protein D1 involved in snRNA maturation(16.27/24)
M256 A10	YGR075C	RNA splicing factor (26.65/37)
M46 B1	YGR076C	Mitochondrial ribosomal protein MRPL25 (YmL25) (17.30/30)
M184 D4	YGR078C	Polypeptide 3 of a Yeast Non-native Actin Binding Complex homolog of a component of the bovine NABC complex (21.92/30)
M256 E6	YGR080W	(36.63/44)
M184 H7	YGR081C	(23.13/33)

M184 A9	YGR082W	20 kDa mitochondrial outer membrane protein import receptor (20.24/20)
M46 B7	YGR083C	translational repressor of GCN4 protein (71.64/90)
M185 E3	YGR103W	(66.66/66)
M185 B7	YGR106C	(29.28/42)
M185 A2	YGR109C	B-type cyclin (41.83/47)
M185 G2	YGR110W	(49.06/50)
M186 B5	YGR112W	Mitochondrial protein necessary for respiration (42.9/50)
M185 G3	YGR119C	Contains GLFG repeats in N-terminal half and heptad repeats in C-terminal half (59.54/62)
M185 H4	YGR120C	(30.38/40)
M185 D7	YGR122W	(44.33/54)
M186 C1	YGR124W	asparagine synthetase (63.03/63)
M186 C4	YGR127W	(34.43/40)
M185 C6	YGR129W	(23.76/34)
M185 E7	YGR130C	(89.79/110)
M185 C1	YGR132C	Prohibitin(31.60/40)
M186 D4	YGR135W	proteasome component Y13 (28.49/36)
M185 B5	YGR136W	(26.62/58)
M55 A4	YGR137W	(13.75/15)
M185 C5	YGR144W	component of the biosynthetic pathway producing the thiazole precursor of thiamine(35.97/60)
M185 E6	YGR145W	(77.88/70)
M185 H8	YGR147C	N alpha-acetyltransferase that acts on methionine termini (31.71/35)
M54 D1	YGR148C	Ribosomal protein RPL30B (rp29) (YL21) (17.08/20)
M54 A5	YGR152C	GTP-binding protein of the ras superfamily involved in bud site selection(29.95/38)
M185 F6	YGR153W	(23.98/34)
M186 G7	YGR154C	(39.29/50)

M55 D5	YGR155W	Cystathionine beta-synthase (55.88/55)
M55 E1	YGR156W	(46.86/45)
M185 C3	YGR158C	(27.53/34)
M186 F4	YGR159C	nuclear localization sequence binding protein (45.57/64)
M186 F5	YGR160W	(22.44/48)
M185 G6	YGR161C	(28.96/38)
M186 H8	YGR163W	(37.62/45)
M185 D4	YGR167W	Clathrin light chain (25.74/28)
M185 H6	YGR169C	(44.47/60)
M54 G6	YGR171C	mitochondrial methionyl-tRNA synthetase (63.38/63)
M55 G1	YGR172C	(27.31/30)
M185 D3	YGR174C	Ubiquinol-cytochrome c reductase assembly factor (18.73/27)
M185 A7	YGR177C	Alcohol acetyltransferase (58.88/66)
M185 C8	YGR178C	(79.45/79)
M277 A1	YGR180C	Ribonucleotide Reductase (37.98/48)
M276 C2	YGR181W	(11.66/14)
M276 B3	YGR182C	(12.90/17)
M277 F6	YGR185C	tyrosyl-tRNA synthetase cytoplasmic (43.47/50)
M276 C8	YGR187C	(43.47/51)
M276 D2	YGR189C	(55.80/55)
M255 C5	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase 3 (36.55/47)
M277 E5	YGR192C	Glyceraldehyde-3-phosphate dehydrogenase 3 (36.55/48)
M276 E6	YGR193C	Protein X component of mitochondrial pyruvate dehydrogenase complex (45.13/63)
M276 D7	YGR194C	(66.03/64)
M277 B1	YGR196C	(89.90/115)

M276 E2	YGR197C	involved in nitrosoguanidine resistance (60.20/63)
M277 F3	YGR198W	(89.98/98)
M276 E7	YGR202C	phosphorylcholine transferase\ or cholinephosphate cytidyltransferase (46.67/58)
M276 E8	YGR203W	(16.49/20)
M277 C1	YGR204W	C1-5 6 7 8-tetrahydrofolate synthase (104.27/105)
M276 F2	YGR205W	(32.01/37)
M56 H5	YGR210C	(45.24/50)
M276 F8	YGR211W	(53.57/70)
M276 D1	YGR212W	(51.59/52)
M276 D4	YGR215W	(12.54/16)
M277 G4	YGR219W	(12.21/16)
M276 E1	YGR220C	Mitochondrial ribosomal protein MRPL9 (YmL9) (E. coli L3) (human MRL3) (29.62/35)
M276 E4	YGR223C	(49.31/53)
M276 F1	YGR228W	(12.65/13)
M277 A3	YGR229C	57 kDa nuclear protein (55.58/55)
M276 F3	YGR230W	(15.28/20)
M276 F5	YGR232W	(25.29/26)
M276 H7	YGR234W	Flavo-hemoglobin(44/48)
M276 H8	YGR235C	(25./6636)
M276 G4	YGR239C	(31.71/38)
M277 B6	YGR240C	phosphofructokinase alpha subunit (108.60/108)
M276 A8	YGR242W	(11.33/13)
M276 A9	YGR243W	(16.27/18)
M276 H1	YGR244C	(47.00/50)
M276 H3	YGR246C	RNA polymerase III transcription factor with homology to TFIIIB (65.59/90)
M276 H4	YGR247W	(26.4/35)
M276 H5	YGR248W	Similar to SOL3 (28.26/36)
M277 C7	YGR249W	(50.27/60)
M276 B8	YGR250C	(85.94/100)
M276 B9	YGR251W	(21.67/35)

M265 D4	YGR252W	positive regulator of GCN4 expression and activity of the HAP2-HAP3-HAP4 transcriptional activation complex (48.4/56)
M276 H2	YGR253C	Proteasome subunit (28.63/36)
M202 B4	YGR254W	enolase I (48.28/55)
M276 A5	YGR255C	COQ6 monooxygenase (52.72/53)
M276 A6	YGR256W	6-phosphogluconate dehydrogenase (54.23/55)
M276 A7	YGR257C	(40.39/47)
M276 C9	YGR259C	(16.09/19)
M276 A4	YGR262C	(28.74/35)
M277 E6	YGR264C	methionyl tRNA synthetase (82.64/84)
M276 D9	YGR267C	GTP-cyclohydrolase I (26.76/35)
M56 G1	YGR268C	(21.81/25)
M276 A3	YGR269W	(11.99/17)
M301 F2	YGR274C	Component of the TAFII complex required for activated transcription (117.39/120)
M277 F9	YGR275W	(20.57/31)
M260 D2	YGR277C	(33.58/42)
M260 G3	YGR278W	(63.58/64)
M190 A5	YGR279C	(42.49/51)
M49 H3	YGR280C	(29.84/45)
M260 B1	YGR284C	(34.13/35)
M260 E2	YGR285C	Zuotin putative Z-DNA binding protein (47.66/55)
M190 G3	YGR286C	Biotin synthase (41.38/49)
M190 B5	YGR287C	(64.82/64)
M260 F6	YGR288W	(52.14/60)
M190 H3	YGR294W	(13.31/18)
M190 H8	YHL002W	(49.83/60)
M260 E10	YHL003C	(45.24/45)
M260 D1	YHL004W	mitochondrial ribosomal protein (43.45/48)

M260 E5	YHL007C	putative serine/threonine protein kinase (103.32/125)
M190 F7	YHL009C	(36.33/48)
M260 E1	YHL012W	(54.34/57)
M190 H2	YHL013C	(33.80/48)
M260 H2	YHL013C	(33.80/45)
M190 E5	YHL015W	(13.42/19)
M260 E9	YHL018W	(13.31/18)
M190 E10	YHL019C	homologous to the medium chain of mammalian clathrin-associated protein complex (66.58/64)
M190 F1	YHL020C	negative regulator of phospholipid biosynthesis (44.47/50)
M260 A3	YHL021C	(51.28/51)
M260 D4	YHL022C	meiotic recombination protein (43.81/52)
M260 B7	YHL024W	(78.54/85)
M190 H7	YHL025W	transcriptional regulator (36.63/50)
M260 H10	YHL027W	Rim101 protein is similar to the Aspergillus pH-response regulator PacC (68.86/80)
M260 B3	YHL029C	(74.72/75)
M190 G5	YHL031C	(24.56/30)
M190 A8	YHL033C	Ribosomal protein RPL4A (rp6) (YL5) (human L7a) (mouse L7a) (rat L7a) (RPL4A and RPL4B code for nearly identical proteins) (28.29/32)
M260 G9	YHL034C	(32.47/44)
M260 H5	YHL039W	(64.46/75)
M260 H9	YHL042W	(16.61/20)
M49 E1	YHL044W	(25.96/30)
M260 F4	YHL046C	(13.33/22)

M260 E7	YHL048W	Protein with similarity to subtelomerically-encoded proteins such as Cos5p Ybr302p Cos3p Cos1p Cos4p Cos8p Cos6p Cos9p (42.02/45)
M190 C8	YHL049C	(29.84/38)
M190 F9	YHL050C	1414-2866(76.78/98)
M260 B11	YHR001W	(48.28/52)
M260 E3	YHR002W	(39.48/59)
M260 B10	YHR007C	cytochrome P450 lanosterol 14a-demethylase (58.33/60)
M190 A11	YHR008C	Manganese-containing superoxide dismutase (25.66/33)
M190 B2	YHR009C	(57.56/58)
M260 H4	YHR011W	(49.27/50)
M260 C6	YHR012W	168-968(31.13/47)
M49 F4	YHR013C	subunit of the major N alpha-acetyltransferase (26.21/30)
M260 H8	YHR014W	(32.12/42)
M260 D11	YHR016C	216-1575(51.59/55)
M260 C2	YHR017W	(42.46/55)
M190 F3	YHR018C	argininosuccinate lyase (50.96/53)
M190 H4	YHR019C	Asparaginyl-tRNA synthetase (60.97/60)
M260 D6	YHR020W	(75.79/85)
M190 F8	YHR022C	(28.29/35)
M188 A1	YHR025W	homoserine synthase (39.48/39)
M261 G3	YHR027C	(109.2/125)
M188 B5	YHR029C	(32.47/36)
M261 A8	YHR030C	putative protein kinase (53.37/58)
M188 B1	YHR033W	(46.64/50)
M261 D5	YHR036W	(51.92/60)
M261 G6	YHR037W	delta-l-pyrroline-5-carboxylate dehydrogenase (63.46/58)
M188 C7	YHR039B C	(12.65/18)
M61 C1	YHR040W	(40.47/50)

M188 C1	YHR040W	(40.47/40)
M261 E5	YHR043C	(27.09/34)
M61 B7	YHR045W	(61.71/45)
M61 D1	YHR048W	(56.65/60)
M188 A3	YHR049W	(26.84/35)
M188 E6	YHR052W	(41.47/41)
M261 F9	YHR053C	copper-binding metallothionein (6.746/15)
M261 B11	YHR054C	(38.97/36)
M261 E1	YHR055C	copper-binding metallothionein (6.746/18)
M261 C4	YHR057C	Peptidylprolyl isomerase (cyclophilin) ER or secreted (22.58/32)
M188 B4	YHR058C	(32.48/38)
M188 F6	YHR060W	required for V-ATPase activity (20.02/30)
M188 F7	YHR061C	(34.57/38)
M261 C11	YHR062C	Protein subunit of nuclear ribonuclease P (RNase P) (32.36/42)
M61 E2	YHR064C	Hsp70 Protein (62.95/64)
M261 D4	YHR065C	(59.76/60)
M261 C7	YHR067W	(30.91/30)
M188 A9	YHR070W	(55/55)
M261 G1	YHR071W	PHO85 cyclin (25./333)
M188 D4	YHR074W	(78.6/598)
M261 D7	YHR075C	(44.03/45)
M261 G8	YHR076W	(41.25/43)
M61 F8	YHR077C	Protein involved in decay of mRNA containing nonsense codons (120.04/120)
M61 F2	YHR079C	putative protein kinase (122.68/40)
M261 A6	YHR081W	(20.45/31)
M261 A2	YHR086W	putative RNA binding protein (57.64/63)
M188 F4	YHR089C	small nucleolar RNP proteins (22.58/30)
M188 A6	YHR090C	(31.05/38)
M261 C6	YHR097C	250-1225(40.47/48)
M261 D10	YHR100C	(20.48/25)

M261 H11	YHR101C	198-1095(36.96/48)
M61 H2	YHR103W	(93.83/90)
M261 A5	YHR104W	(36.08/40)
M261 D6	YHR105W	(23.65/34)
M188 B6	YHR106W	Thioredoxin reductase (37.73/38)
M61 H7	YHR107C	Component of 10 nm filaments of mother-bud neck (septin) (44.80/50)
M261 E10	YHR108W	(64.46/64)
M188 F9	YHR109W	(64.46/64)
M261 F3	YHR111W	(48.51/59)
M261 B5	YHR112C	(41.61/47)
M188 A5	YHR113W	(54.01/54)
M261 H7	YHR114W	(69.74/75)
M261 B9	YHR115C	(45.79/56)
M189 C4	YHR121W	(20.68/32)
M189 B2	YHR127W	(26.84/36)
M189 D3	YHR128W	UPRTase(27.72/36)
M189 A7	YHR132C	ExtraCellular Mutant (47.33/50)
M63 F1	YHR135C	membrane-bound casein kinase I homolog (59.21/60)
M189 E3	YHR136C	17 kDa protein (16.31/28)
M189 D4	YHR137W	aromatic amino acid aminotransferase II (56.54/64)
M189 D5	YHR138C	(12.57/13)
M189 E5	YHR144C	dCMP deaminase (34.45/38)
M191 D10	YHR147C	Mitochondrial ribosomal protein MRPL6 (YmL6) (23.57/32)
M189 E4	YHR151C	(57.89/66)
M191 F1	YHR156C	(37.43/57)
M191 A8	YHR161C	(70.10/80)
M64 G4	YHR163W	weak multicopy suppressor of los1-1 (30.91/32)
M191 D5	YHR167W	(28.82/35)
M189 E6	YHR169W	(47.52/50)
M310 F3	YHR170W	putative Upf1p-interacting protein (57.09/64)
M64 H4	YHR171W	(69.41/64)

M255 F5	YHR172W	Spindle Pole Body component with an molecular weight of 97 kDa(90.64/100)	M194 C1	YIL022W	48.8 kDa protein involved in mitochondrial protein import (47.52/50)
M189 G3	YHR174W	enolase(48.28/48)	M65 F3	YIL026C	Irregular(126.53/50)
M189 F6	YHR177W	(49.94/52)	M192 D6	YIL027C	(15.54/20)
M189 C8	YHR179W	NAPDH dehydrogenase (old yellow enzyme) isoform 2 (44.11/50)	M192 E4	YIL033C	regulatory subunit of cAMP-dependent protein kinase (45.79/55)
M191 D4	YHR182W	(86.46/86)	M65 E1	YIL038C	General negative regulator of transcription\ may inhibit RNA polymerase II transcription machinery (91.99/60)
M63 G3	YHR183W	Phosphogluconate Dehydrogenase (Decarboxylating) (53.9/50)	M192 F3	YIL040W	(15.39/22)
M189 G1	YHR188C	(67.13/67)	M65 G2	YIL041W	(35.97/20)
M189 H5	YHR192W	(30.69/36)	M192 E5	YIL042C	(43.47/50)
M191 E8	YHR193C	GAL4 enhancer protein homolog of human alpha NAC subunit of the nascent-polypeptide-associated complex (19.17/34)	M310 G3	YIL043C	cytochrome b reductase (35.45/42)
M191 B11	YHR195W	(35.42/40)	M192 D9	YIL053W	DL-glycerol-3-phosphatase(29.92/38)
M191 H1	YHR196W	(63.46/66)	M194 E4	YIL057C	(18.07/20)
M189 B5	YHR199C	(34.13/38)	M194 D2	YIL063C	Yeast Ran-Binding protein 2 (36.00/40)
M191 F8	YHR201C	Cytosolic exopolyphosphatase (43.70/43)	M192 G3	YIL064W	(28.48/36)
M191 G9	YHR202W	(66.33/40)	M192 F9	YIL069C	413-817 40S ribosomal protein S24E (RP50) (14.96/18)
M189 B3	YHR205W	cAMP-dependent protein kinase homolog suppressor of cdc25ts (90.75/98)	M65 G1	YIL070C	(29.39/36)
M189 B4	YHR206W	(68.53/68)	M65 A2	YIL071W	(/35)
M191 A6	YHR207C	(57.89/67)	M192 D8	YIL076W	(3/9.649)
M189 A6	YHR208W	Branched-Chain Amino Acid Transaminase (43.34/48)	M192 G9	YIL077C	(35/2339)
M191 G8	YHR209W	(32.12/32)	M192 B5	YIL082W	(32./0140)
M191 H9	YHR210C	(37.54/48)	M192 B7	YIL083C	(40.2/848)
M194 G1	YHR213W	(21.89/32)	M67 A1	YIL086C	(11.35/16)
M194 G3	YHR214W	(22.44/34)	M67 D2	YIL087C	(17.30/20)
M65 C4	YHR216W	(57.64/60)	M195 A4	YIL089W	(22.66/33)
M65 C3	YIL003W	(32.34/32)	M67 A9	YIL093C	(29.07/30)
M194 H3	YIL010W	(23.76/36)	M67 B1	YIL094C	(40.84/50)
M192 F7	YIL020C	(28.74/36)	M67 E2	YIL095W	probable serine/threonine-protein kinase (89.21/90)
			M195 A3	YIL096C	(36.99/50)
			M195 B4	YIL097W	(56.87/60)
			M67 E5	YIL098C	(17.08/17)

M67 F6	YIL099W	intracellular glucoamylase (60.5/60)
M195 A2	YIL103W	(46.86/56)
M195 B3	YIL104C	(55.80/55)
M195 C4	YIL105C	(75.49/75)
M195 A5	YIL106W	Mps One Binder (26.07/28)
M195 A6	YIL107C	6-Phosphofructose-2- kinase(91.00/100)
M195 B2	YIL111W	90-544 Cytochrome-c oxidase chain Vb (16.72/20)
M255 A6	YIL113W	(23.1/33)
M195 B5	YIL114C	voltage dependent anion channel (YVDAC2) (30.94/40)
M195 B7	YIL116W	histidinol-phosphate aminotransferase (42.46/54)
M67 D9	YIL117C	(35.01/35)
M67 E1	YIL118W	ras homolog--GTP binding protein (25.52/30)
M195 C2	YIL119C	inhibitor of ras (44.80/54)
M66 D4	YIL122W	(38.72/38)
M195 C7	YIL124W	(32.78/45)
M67 E9	YIL125W	alpha-ketoglutarate dehydrogenase (111.65/116)
M195 D2	YIL127C	(22.69/38)
M195 B6	YIL131C	(53.37/38)
M195 D7	YIL132C	(23.46/33)
M66 F1	YIL134W	mitochondrial inner membrane carrier protein for FAD (34.32/36)
M195 D3	YIL136W	45-kDa mitochondrial outer membrane protein (43.34/43)
M66 E4	YIL138C	Tropomyosin isoform 2 (17.74/17)
M67 G9	YIL141W	(14.3/14)
M195 E1	YIL142W	Cytoplasmic chaperonin of the Cct ring complex related to Tcp1p\ subunit beta (58.08/65)
M67 H3	YIL144W	(76.12/80)

M67 C7	YIL147C	histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade and is similar to bacterial two-component regulators (134.23/135)
M67 H9	YIL149C	(184.72/185)
M195 E3	YIL152W	(25.96/34)
M66 B4	YIL153W	(43.34/43)
M196 G5	YIL154C	Protein involved in nucleo-mitochondrial control of maltose galactose and raffinose utilization(38.09/38)
M195 D6	YIL155C	glycerol-3-phosphate dehydrogenase mitochondrial (71.42/40)
M67 F8	YIL156W	Ubiquitin-specific protease (117.92/117)
M195 F3	YIL160C	peroxisomal 3- oxoacyl CoA thiolase (45.90/55)
M196 H5	YIL162W	invertase (sucrose hydrolyzing enzyme) (58.63/64)
M196 B8	YIL164C	(21.92/32)
M67 E7	YIL171W	(12.1/12)
M67 C2	YIL174W	(8.46/8)
M67 D4	YIL176C	(13.23/20)
M195 G5	YIR001C	(27.53/38)
M67 H8	YIR003W	(74.8/75)
M195 A9	YIR004W	(47.63/89)
M197 B2	YIR006C	PAB-dependent poly(A) ribonuclease (162.83/180)
M310 H3	YIR007W	(84.15/94)
M198 B4	YIR008C	p48 polypeptide of DNA primase (45.02/55)
M197 B7	YIR010W	(63.47/70)
M68 C7	YIR011C	restores protein transport when overexpressed and rRNA stability to a sec23 mutation (35.12/40)
M69 C5	YIR012W	(47.52/50)
M69 B1	YIR014W	(30.47/36)

M198 G5	YIR017C	Transcriptional activator of sulfur amino acid metabolism (20.60/32)	M197 A9	YJL031C	Geranylgeranyltransferase Type II alpha subunit (PGGTase-II alpha subunit) (31.93/40)
M197 C7	YIR018W	(27.06/40)	M197 E4	YJL035C	(27.53/37)
M69 A4	YIR026	nitrogen starvation induced protein phosphatase (40.07/48)	M197 H5	YJL036W	(46.64/50)
M198 H7	YIR027C	allantoinase(50.63/52)	M68 G2	YJL043W	(28.48/40)
M197 D1	YIR029W	allantoicase(37.84/48)	M197 D10	YJL049W	(49.61/60)
M197 E2	YIR030C	(26.87/33)	M197 F2	YJL052W	Glyceraldehyde-3-phosphate dehydrogenase 1 (36.63/45)
M198 E4	YIR032C	ureidoglycolate hydrolase (21.48/34)	M197 A7	YJL054W	(52.69/34)
M197 E7	YIR034C	saccharopine dehydrogenase (41.06/48)	M197 B8	YJL055W	(27.06/36)
M68 E7	YIR035C	(27.97/36)	M268 B2	YJL059W	Homolog of human CLN3 (44.99/45)
M197 F9	YIR036C	(28.96/34)	M199 F4	YJL061W	82-kDa protein with putative coiled-coil domain has carboxy-terminal domain containing heptad repeats that binds Nsp1p nucleoporin (78.54/80)
M197 E1	YIR037W	putative glutathione-peroxidase (18.04/33)	M268 C5	YJL062W	(91.41/98)
M197 F2	YIR038C	(25.77/35)	M199 E9	YJL065C	(18.40/35)
M197 F7	YIR042C	(25.99/35)	M199 B1	YJL066C	(27.75/40)
M197 A4	YJL003W	(13.09/18)	M199 F9	YJL073W	DnaJ-like protein of the endoplasmic reticulum membrane (76.23/70)
M68 E4	YJL004C	Multicopy suppressor of ypt6 null mutation (22.46/30)	M199 B7	YJL079C	Similar to plant PR-1 class of pathogen related proteins (32.92/60)
M197 H9	YJL008C	Component of Chaperonin Containing T-complex subunit eight (62.51/62)	M199 D1	YJL082W	(80.52/80)
M197 B4	YJL011C	(17.74/27)	M268 E2	YJL083W	(66.55/74)
M310 A4	YJL013C	Checkpoint protein required for cell cycle arrest in response to loss of microtubule function (56.68/65)	M71 B3	YJL084C	(115.09/80)
M197 H7	YJL014W	Cytoplasmic chaperonin subunit gamma (58.85/60)	M199 E8	YJL088W	Ornithine carbamoyltransferase (48.51/40)
M69 F5	YJL016W	(18.92/28)	M268 D1	YJL090C	(84.07/98)
M197 C4	YJL019W	(68.31/70)	M199 F8	YJL096W	(24.75/30)
M68 G5	YJL021C	(40.28/50)	M268 D9	YJL097W	(23.98/29)
M197 A2	YJL025W	(56.65/60)	M199 G3	YJL100W	(66.88/70)
M68 H5	YJL029C	(90.45/90)	M265 E5	YJL103C	(68.01/70)
M69 D4	YJL030W	putative calcium binding protein (21.67/32)	M199 G8	YJL104W	(16.5/20)
			M268 E9	YJL105W	(61.71/64)

M268 F1	YJL106W	Homolog of the human core snRNP protein E\ Serine/Threonine kinase(71.06/88)
M268 G5	YJL110C	GATA zinc finger protein 3 (60.64/70)
M71 A5	YJL111W	(60.61/60)
M71 F5	YJL112W	(78.65/80)
M268 G1	YJL114W	(45.65/52)
M71 D2	YJL115W	Anti-silencing protein that causes depression of silent loci when overexpressed (30.8/50)
M268 A3	YJL115W	Anti-silencing protein that causes depression of silent loci when overexpressed (30.8/46)
M71 H3	YJL117W	Putative inorganic phosphate transporter (34.32/40)
M199 H1	YJL122W	(19.46/28)
M71 E2	YJL123C	(52.61/50)
M199 B4	YJL124C	(18.95/32)
M70 G3	YJL126W	(33.88/40)
M268 G8	YJL128C	protein kinase homolg (73.51/80)
M199 D3	YJL131C	(39.19/48)
M199 E5	YJL133W	mitochondrial carrier protein (34.65/40)
M71 F1	YJL138C	translation initiation factor (43.48/44)
M268 D3	YJL139C	(47.11/53)
M199 D4	YJL140W	fourth-largest subunit of RNA polymerase II (24.42/34)
M199 A8	YJL143W	16.5 kDa inner membrane protein required for import of mitochondrial precursor proteins (17.49/20)
M70 E6	YJL145W	(32.45/36)
M199 B2	YJL146W	IME2-Dependent Signalling (51.7/30)
M199 F3	YJL147C	(42.05/47)
M199 E4	YJL148W	RNA polymerase I subunit not shared (A34.5) (25.74/40)
M199 B8	YJL151C	(14.66/28)

M201 D2	YJL155C	Fructose-2 6-bisphosphatase (49.75/55)
M73 H3	YJL156C	(75.60/80)
M201 B5	YJL157C	Factor arrest protein (91.33/98)
M73 G5	YJL158C	Protein with homology to Hsp150p and Pir1p Pir2p and Pir3p (25.00/60)
M73 B1	YJL162C	(53.05/64)
M200 D6	YJL166W	Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein) (10.45/12)
M201 B7	YJL167W	Farnesyl diphosphate synthetase (FPP synthetase) (38.83/48)
M201 B1	YJL170C	An a-specific gene that is induced to a higher expression level by alpha factor (20.26/28)
M201 B4	YJL172W	carboxypeptidase yscS (63.47/75)
M72 D5	YJL174W	(30.47/34)
M201 C7	YJL175W	(18.81/28)
M73 F8	YJL176C	transcription factor (90.78/90)
M72 C1	YJL178C	(21.59/28)
M73 B4	YJL180C	(35.78/36)
M201 D5	YJL181W	(67.32/67)
M73 G8	YJL184W	(13.64/20)
M200 E1	YJL186W	(64.57/77)
M73 C6	YJL190C	Ribosomal protein RPS24 (14.33/16)
M73 H8	YJL192C	(25.77/50)
M201 A3	YJL195C	(25.66/25)
M73 A9	YJL200C	(86.82/45)
M200 C3	YJL203W	RNA splicing factor (30.91/43)
M72 F8	YJL208C	mitochondrial nuclease (36.22/42)
M201 G1	YJL210W	Required for peroxisome biogenesis (29.92/32)
M201 C3	YJL211C	(16.20/22)
M200 A2	YJL218W	(21.67/31)
M201 G7	YJL223C	(13.23/20)

M73 B2	YJR002W	(65.34/70)
M201 A2	YJR002W	(65.34/80)
M72 C6	YJR006W	(53.68/55)
M72 E7	YJR007W	Translation initiation factor eIF-2 alpha subunit (33.55/40)
M72 H8	YJR008W	(37.39/42)
M255 E6	YJR009C	glyceraldehyde 3-phosphate dehydrogenase (36.55/50)
M201 F3	YJR010W	ATP sulfurylase (56.32/68)
M73 A5	YJR011C	(28.74/35)
M201 G5	YJR012C	(22.80/34)
M200 D8	YJR014W	(21.89/34)
M72 C10	YJR016C	dihydroxyacid dehydratase (64.48/64)
M201 C2	YJR017C	Peptidyl-prolyl cis/trans isomerase (PPIase) (20.93/33)
M201 A5	YJR019C	peroxisomal acyl-CoA thioesterase (38.42/45)
M200 E8	YJR022W	(14.29/22)
M206 A1	YJR025C	3-hydroxyanthranilic acid dioxygenase (19.50/34)
M205 B2	YJR026W	(48.51/50)
M205 E4	YJR028W	(48.51/55)
M205 C2	YJR034W	Required for assembly of active cytochrome c oxidase (11.99/16)
M205 D3	YJR043C	(38.53/47)
M205 G5	YJR045C	Mitochondrial matrix protein involved in protein import\ subunit of Scl endonuclease(71.97/72)
M205 B7	YJR046W	(66.55/75)
M205 G9	YJR048W	iso-1-cytochrome c (12.1/16)
M205 C1	YJR049C	(58.33/64)
M205 E3	YJR051W	osmotic growth protein (55.22/60)
M205 F4	YJR052W	(62.36/64)
M205 C7	YJR054W	(54.78/55)

M205 E8	YJR055W	Protein required for growth at high temperature (18.25/32)
M205 H9	YJR056C	(25.99/36)
M205 D1	YJR057W	thymidylate kinase (23.87/33)
M202 B5	YJR060W	basic helix-loop-helix protein (38.72/38)
M205 A6	YJR061W	(102.96/100)
M205 D7	YJR062C	52-kDa amidase specific for N-terminal asparagine and glutamine (50.30/50)
M205 F3	YJR067C	(15.54/25)
M205 B6	YJR069C	(21.70/33)
M205 E7	YJR070C	(35.78/45)
M52 D2	YJR074W	(24.09/32.0)
M205 G3	YJR075W	putative mannosyltransferase (43.67/44)
M52 E4	YJR076C	Component of 10 nm filaments of mother-bud neck (45.68/50)
M52 E5	YJR077C	mitochondrial protein import receptor (34.24/38)
M205 F7	YJR078W	(49.94/50)
M205 C10	YJR080C	(43.47/40)
M205 F1	YJR080C	(12.46/20)
M205 G2	YJR083C	(34.02/63)
M205 D6	YJR086w	gamma subunit of G protein coupled to mating factor receptors (12.21/16)
M205 H8	YJR088C	(32.25/48)
M205 D10	YJR089W	(105.05/100)
M205 B5	YJR093C	(36.00/36)
M303 F3	YJR094C	meiotic gene expression\meiosis inducing protein (39.63/50)
M205 A9	YJR095W	protein related to mitochondrial carriers (35.53/40)
M205 E10	YJR096W	(31.13/35)
M205 B4	YJR099W	ubiquitin hydrolase (26.07/35)
M205 C5	YJR100C	(36.00/37)

M205 F6	YJR101W	(29.47/37)
M205 H7	YJR102C	(22.35/28)
M206 F7	YJR103W	CTP synthase (62.25/48)
M205 H1	YJR105W	(37.51/47)
M205 C4	YJR107W	(36.29/50)
M205 C9	YJR111C	(31.26/36)
M205 G10	YJR112W	(22.22/30)
M205 A2	YJR113C	(27.20/35)
M206 E4	YJR116W	(30.8/34)
M205 A8	YJR118C	(22.46/36)
M205 D9	YJR119C	(80.11/90)
M209 F2	YJR123W	ribosomal protein RPS5 (mammalian S5) (previously called rp14 S2 or YS8)(24.86/30)
M62 D2	YJR125C	(44.91/64)
M209 B1	YJR129C	(37.32/40)
M209 G2	YJR131W	specific alpha- mannosidase (60.5/60)
M53 A4	YJR132W	(115.4/9115)
M208 F4	YJR133W	(23.1/33)
M310 E4	YJR134C	(77.80/98)
M208 E6	YJR135C	Required for maintenance of chromosomes and minichromosomes (26.32/36)
M208 E7	YJR144W	(29.7/36)
M208 C1	YJR145C	271-1042 Ribosomal protein RPS7B (YS6) (rp5) (Rat S4) (human S4) (RPS7A and RPS7B code for identical proteins) (28.82/36)
M209 A3	YJR147W	(39.49/49)
M53 B4	YJR148W	Branched-Chain Amino Acid Transaminase (41.47/45)
M209 D1	YJR153W	(39.82/40)
M208 B2	YJR154W	(38.27/50)
M208 B3	YJR155W	(31.79/40)
M208 A4	YJR156C	Thiamine biosynthetic enzyme (37.43/50)

M209 E1	YJR161C	Protein with similarity to members of the Ybr302p/VYcr007pVC os8pVCos9p family coded from subtelomeric region (42.26/42)
M208 C3	YKL001C	adenylylsulfate kinase (22.35/33)
M208 B4	YKL002W	(16.72/36)
M208 E1	YKL006W	528-815 probable 60S ribosomal protein L14EA (15.39/18)
M209 D2	YKL007W	alpha subunit of capping protein (29.59/38)
M324 C3	YKL009W	(26.07/40)
M208 H5	YKL011C	cruciform cutting endonuclease (38.86/36)
M208 H7	YKL013C	Arp Complex Subunit (18.84/30)
M208 B5	YKL018W	(36.3/48)
M208 A6	YKL019W	CAAX farnesyltransferase alpha subunit (34.87/45)
M208 E2	YKL023W	(30.58/33)
M209 D3	YKL024C	uridine- monophosphate kinase (uridylate kinase) (22.47/34)
M208 C5	YKL026C	(18.40/31)
M208 B6	YKL027w	(49.38/60)
M202 C5	YKL035W	(55/60)
M208 G3	YKL040C	(28./2936)
M208 C4	YKL041W	(24.7/540)
M208 D5	YKL042W	Component of the spindle pole body (40.04/40)
M202 D5	YKL043W	putative transcription factor (40.47/55)
M208 D6	YKL051W	(38.94/47)
M209 H6	YKL052C	(32.25/48)
M58 A1	YKL055C	(30.61/33)
M58 B2	YKL056C	(18.40/20)
M58 B3	YKL059C	(48.54/58)
M59 E6	YKL060C	aldolase(39.52/39)
M210 E6	YKL061W	(12.54/16)
M210 F1	YKL063C	(18.40/30)

M210 D3	YKL065C	Yeast endoplasmic reticulum 25 kDa transmembrane protein (22.69/30)
M210 H4	YKL067W	Nucleoside diphosphate kinase (16.94/28)
M210 B1	YKL070W	(18.7/29)
M58 C1	YKL071W	(28.37/45)
M59 A5	YKL074C	involved in early pre-mRNA splicing (58.00/60)
M59 F5	YKL075C	(49.53/64)
M59 G7	YKL077W	(43.23/55)
M211 C4	YKL081W	532-1565 Translation elongation factor EF-1gamma (45.43/48)
M210 H1	YKL087C	cytochrome c1 heme lyase (24.67/37)
M58 C2	YKL088W	(62.92/70)
M210 F4	YKL090W	(48.84/64)
M210 F6	YKL093W	(37.4/55)
M59 B1	YKL094W	(34.54/45)
M210 F2	YKL096W	cell wall mannoprotein (26.4/50)
M211 E3	YKL103C	vacuolar aminopeptidase ysc1 (56.57/64)
M59 A6	YKL106W	aspartate aminotransferase mitochondrial (49.72/50)
M210 G5	YKL107W	(34.1/40)
M202 F5	YKL109W	transcriptional activator protein of CYC1 (component of HAP2VHAP3 heteromer) (61.05/70)
M210 G6	YKL116C	(57.01/70)
M210 A3	YKL119C	25.2 kDa protein involved in assembly of vacuolar H(+) ATPase (23.68/34)
M59 C6	YKL122C	(18.40/20)
M210 H6	YKL124W	suppressor of SHR3 (63.8/100)
M210 A7	YKL132C	(47.33/55)
M210 B2	YKL134C	(84.73/98)
M210 B7	YKL140W	succinate dehydrogenase cytochrome b subunit (60.49/64)

M210 C2	YKL142W	mitochondrial ribosomal protein (24.2/36)
M269 A1	YKL149C	debranching enzyme (44.58/50)
M213 G1	YKL150W	NADH-cytochrome b5 reductase (33.33/38)
M269 A3	YKL151C	(37.10/49)
M269 D4	YKL152C	Phosphoglycerate mutase (27.20/35)
M213 G4	YKL153W	(18.7/30)
M77 E6	YKL154W	(26.95/30)
M269 F7	YKL156W	354-599 40S ribosomal protein S27-1 (9.13/10)
M213 G2	YKL159C	(23.24/32)
M213 H3	YKL160W	(16.06/36)
M269 F5	YKL161C	(47.66/52)
M78 A8	YKL163W	Protein containing tandem internal repeats (35.86/40)
M77 H3	YKL167C	16 kDa mitochondrial ribosomal large subunit protein (15.10/18)
M213 A4	YKL168C	(80.77/50)
M77 G6	YKL170W	mitochondrial ribosomal protein L14 (15.39/16)
M77 B8	YKL171W	(102.29/?)
M213 B6	YKL172W	(47.08/64)
M77 A4	YKL175W	(55.44/20)
M269 A8	YKL180W	616-861 (20.45/32)
M77 D1	YKL181W	ribose-phosphate pyrophosphokinase (47.08/50)
M213 A3	YKL183W	(33.77/34)
M77 A5	YKL184W	Ornithine decarboxylase (51.47/51)
M78 A7	YKL186C	mRNA transport regulator (20.37/32)
M269 D1	YKL189W	(44/55)
M77 G2	YKL190W	129-604 Type 2B protein phosphatase\ regulatory B subunit of calcineurin (19.46/20)
M78 B4	YKL191W	(58.8/560)
M269 H4	YKL192C	(13.78/14)

M78 H5	YKL193C	Interacts with and may be a positive regulator of GLC7 which encodes type I protein phosphatase (37.21/40)
M77 B7	YKL194C	mitochondrial threonine-tRNA synthetase (50.85/51)
M269 D7	YKL195W	(47.08/58)
M213 C2	YKL206C	(29.40/36)
M213 C4	YKL208W	(29.92/38)
M77 H1	YKL213C	(78.68/70)
M78 B3	YKL214C	(22.46/32)
M213 D4	YKL216W	dihydroorotate dehydrogenase (34.65/40)
M77 B6	YKL217W	carboxylic acid transporter protein homolog (67.87/70)
M77 E7	YKL218C	(35.89/36)
M77 F8	YKL219W	Protein with similarity to subtelomerically-encoded proteins such as Cos5p Ybr302p Cos3p Cos1p Cos4p Cos8p Cos6p Cos9p (44.88/50)
M213 E4	YKL224C	(13.56/16)
M77 F7	YKR001C	putative GTP-binding protein\ similar to mammalian Mx proteins (77.47/80)
M77 F4	YKR006C	mitochondrial ribosomal protein YmL13 (30.38/35)
M213 F4	YKR007W	(20.45/36)
M77 E3	YKR013W	Similar to plant PR-1 class of pathogen related proteins (36.3/60)
M78 G4	YKR014C	(25.77/32)
M77 A9	YKR018C	(79.78/80)
M214 A1	YKR020W	(18.25/34)
M218 G1	YKR021W	(100.76/110)
M76 H3	YKR022C	(35.45/40)
M214 B5	YKR023W	(58.41/68)
M214 C7	YKR025W	(31.13/40)
M75 A4	YKR030W	(30.14/32)
M75 A10	YKR035C	(23.46/23)
M218 B1	YKR036C	CCR4 associated factor (72.52/85)
M76 F2	YKR037C	(32.48/40)

M214 E7	YKR041W	(27.61/36)
M75 B10	YKR043C	(29.84/36)
M76 G2	YKR045C	(21.04/30)
M75 C4	YKR046C	(31.26/36)
M76 A6	YKR048C	nucleosome assembly protein I (45.90/50)
M75 C10	YKR051W	(46.09/48)
M214 D1	YKR052C	mitochondrial carrier protein (33.47/48)
M214 E5	YKR055W	ras homolog--GTP binding protein (32.12/48)
M218 F5	YKR056W	(67.98/67)
M218 E7	YKR058W	(52.91/80)
M75 D10	YKR059W	translation initiation factor (43.56/50)
M218 D1	YKR060W	(30.35/45)
M218 C2	YKR061W	putative mannosyltransferase\ type 2 membrane protein (46.86/58)
M76 D4	YKR062W	Small subunit of TFIIIE transcription factor (36.29/45)
M218 F7	YKR066C	Cytochrome-c peroxidase (39.74/39)
M76 D10	YKR067W	(81.84/43)
M218 D2	YKR069W	siroheme synthase (65.34/65)
M214 D4	YKR070W	(38.83/40)
M214 H6	YKR072C	sit4 suppressor (61.85/61)
M75 C9	YKR074W	(17.26/20)
M214 B10	YKR075C	(33.80/48)
M218 E2	YKR077W	(40.04/50)
M76 F4	YKR078W	(64.46/64)
M310 C5	YKR079C	(92.21/100)
M76 E6	YKR080W	NAD-dependent 5 10-methylenetetrahydrofolate dehydrogenase (35.31/40)
M218 A7	YKR081C	(37.87/52)
M218 E8	YKR083C	(14.66/35)
M75 D3	YKR085C	22.3 kDa mitochondrial ribosomal large subunit protein YmL20\ homologous to L17 of E. coli (21.48/32)
M218 H4	YKR087C	(34.57/44)
M218 F8	YKR091W	(16.83/35)

M214 C8	YKR097W	phosphoenolpyruvate carboxylkinase (60.5/65)
M202 H5	YKR099W	(89.32/110)
M76 F3	YKR101W	repressor of silent mating loci (74.69/35)
M75 C2	YLL002W	(48.07/48)
M218 C6	YLL006W	mitochondrial outer membrane protein (46.97/60)
M218 C7	YLL007C	(73.28/75)
M218 G8	YLL009C	(7.626/10)
M79 D2	YLL011W	nucleolar snRNP protein (53.9/55)
M80 E3	YLL012W	(63.14/63)
M219 E1	YLL019C	protein kinase homolog (81.10/90)
M220 F5	YLL022C	(42.48/53)
M220 B1	YLL026W	heat shock protein 104 (99.99/99)
M219 F1	YLL027W	(27.61/40)
M79 G3	YLL028W	(64.57/63)
M219 H7	YLL033W	(25.41/40)
M219 G1	YLL035W	(69.63/80)
M79 H3	YLL036C	RNA splicing factor (55.46/64)
M219 H5	YLL039C	ubiquitin (41.94/50)
M219 A8	YLL041C	Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit (29.39/34)
M219 H1	YLL043W	Suppressor of tps1Vfdp1 and member of the MIP family of transmembrane channels\ may be involved in glycerol efflux (73.7/81)
M80 D5	YLL045C	Ribosomal protein RPL4B (rp6) (YL5) (human L7a) (mouse L7a) (rat L7a) (RPL4A and RPL4B code for nearly identical proteins) (28.29/36)
M80 F1	YLL050C	194-611 Cofilin actin binding and severing protein (15.84/30)
M80 D9	YLL056C	(32.81/32)

M79 G1	YLL058W	(63.46/64)
M79 C4	YLL060C	(25.66/32)
M219 A7	YLR005W	(50.82/60)
M79 E9	YLR006C	Two-component signal transducer that with Sln1p regulates osmosensing MAP kinase cascade(suppressor of sensor kinase) (78.45/78)
M79 E4	YLR009W	(22/32)
M219 D4	YLR010C	(17./6330)
M219 D5	YLR011W	(21.1/230)
M219 D1	YLR015W	(55.66/64)
M219 D2	YLR016C	(22.47/40)
M219 D3	YLR017W	Protein that regulates ADH2 gene expression (37.18/48)
M219 E5	YLR019W	(43.78/50)
M219 E8	YLR022C	(27.53/38)
M80 A6	YLR026C	Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Golgi transport. (37.43/25)
M219 F5	YLR027C	aspartate aminotransferase cytosolic (47.55/50)
M79 F8	YLR029C	Ribosomal protein RPL13A (YL10A) (rat L15) (22.47/30)
M219 F8	YLR030W	(29.04/40)
M80 C2	YLR031W	(20.57/32)
M219 F3	YLR033W	(55.33/55)
M219 F6	YLR036C	(22.46/33)
M80 B10	YLR037C	(13.67/13)
M223 E1	YLR040C	(24.67/38)
M82 C6	YLR043C	thioredoxin (11.46/12)
M81 F7	YLR044C	pyruvate decarboxylase (61.96/62)
M82 D6	YLR051C	(23.90/30)
M222 G7	YLR053C	(11.91/22)
M82 C10	YLR054C	(56.45/56)
M223 B1	YLR055C	transcription factor (66.35/70)
M81 D2	YLR056W	C-5 sterol desaturase (40.36/55)
M81 H3	YLR057W	(93.5/98)

M81 D5	YLR058C	serine hydroxymethyltransferase (51.62/55)	M222 D7	YLR124W	(12.65/16)
M82 E6	YLR059C	(29.62/30)	M222 F8	YLR125W	(15.07/40)
M81 H7	YLR060W	Phenylalanyl-tRNA synthetase alpha subunit cytoplasmic (65.56/65)	M82 A2	YLR127C	APC (anaphase promoting complex) component (93.86/94)
M82 H8	YLR061W	402-755 (13.42/28)	M82 D7	YLR131C	activator of CUP1 expression (84.73/40)
M222 A5	YLR066W	signal peptidase subunit (20.45/34)	M222 E7	YLR132C	(31.93/40)
M222 H3	YLR073C	(22.03/34)	M221 A3	YLR137W	(40.48/52)
M81 E5	YLR074C	(18.39/28)	M84 C6	YLR139C	(70.76/70)
M222 A6	YLR075W	Ubiquinol-cytochrome C reductase complex subunit VI requiring protein (24.42/33)	M86 G9	YLR141W	Upstream activation factor subunit (40.04/55)
M82 A8	YLR076C	(15.43/16)	M221 E6	YLR142W	proline oxidase (52.47/60)
M222 H7	YLR077W	(64.24/67)	M84 C2	YLR144C	Identified as an activity necessary for actin polymerization in permeabilized cells (85.72/90)
M81 D1	YLR079W	P40 inhibitor of Cdc28p-Clb5 protein kinase complex (31.45/50)			
M223 G3	YLR082C	Smc4 protein member of SMC family (43.25/55)	M79 E4	YLR009W	(22/32)
M222 B6	YLR083C	integral membrane protein\ p24a protein (73.40/90)	M219 D4	YLR010C	(17./6330)
M222 B4	YLR089C	(65.25/65)	M219 D5	YLR011W	(21.1/230)
M81 G5	YLR090W	Homolog of E. coli DnaJ closely related to Ydj1p (50.6/60)	M219 D1	YLR015W	(55.66/64)
M81 H6	YLR091W	(32.34/40)	M219 D2	YLR016C	(22.47/40)
M222 B8	YLR093C	(27.64/39)	M219 D3	YLR017W	Protein that regulates ADH2 gene expression (37.18/48)
M223 H2	YLR097C	(37.87/52)	M219 E5	YLR019W	(43.78/50)
M81 H5	YLR098C	DNA binding activator (71.31/75)	M219 E8	YLR022C	(27.53/38)
M222 D6	YLR099C	(43.47/48)	M80 A6	YLR026C	Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Golgi transport. (37.43/25)
M82 C8	YLR100W	(38.38/?)			
M81 A11	YLR102C	(29.28/45)	M219 F5	YLR027C	aspartate aminotransferase cytosolic (47.55/50)
M82 F1	YLR103C	omosomal DNA replication initiation protein (71.53/?)			
M222 E6	YLR107W	(44.55/48)	M79 F8	YLR029C	Ribosomal protein RPL13A (YL10A) (rat L15) (22.47/30)
M222 D8	YLR109W	(19.47/38)			
M81 G4	YLR113W	mitogen-activated protein kinase (MAP kinase) (47.96/60)	M219 F8	YLR030W	(29.04/40)
M81 A6	YLR114C	(84.07/100)	M80 C2	YLR031W	(20.57/32)
M223 D1	YLR119W	suppressor of mal-1 mutation (23.54/33)	M219 F3	YLR033W	(55.33/55)
			M219 F6	YLR036C	(22.46/33)
			M80 B10	YLR037C	(13.67/13)
			M223 E1	YLR040C	(24.67/38)
			M82 C6	YLR043C	thioredoxin (11.46/12)

M81 F7	YLR044C	pyruvate decarboxylase (61.96/62)
M82 D6	YLR051C	(23.90/30)
M222 G7	YLR053C	(11.91/22)
M82 C10	YLR054C	(56.45/56)
M223 B1	YLR055C	transcription factor (66.35/70)
M81 D2	YLR056W	C-5 sterol desaturase (40.36/55)
M81 H3	YLR057W	(93.5/98)
M81 D5	YLR058C	serine hydroxymethyltransferase (51.62/55)
M82 E6	YLR059C	(29.62/30)
M81 H7	YLR060W	Phenylalanyl-tRNA synthetase alpha subunit cytoplasmic (65.56/65)
M82 H8	YLR061W	402-755 (13.42/28)
M222 A5	YLR066W	signal peptidase subunit (20.45/34)
M222 H3	YLR073C	(22.03/34)
M81 E5	YLR074C	(18.39/28)
M81 E5	YLR074C	(18.39/28)
M222 A6	YLR075W	Ubiquinol-cytochrome C reductase complex subunit VI requiring protein (24.42/33)
M222 A6	YLR075W	Ubiquinol-cytochrome C reductase complex subunit VI requiring protein (24.42/33)
M82 A8	YLR076C	(15.43/16)
M222 H7	YLR077W	(64.24/67)
M223 G5	YLR077W	(64.24/60)
M81 D1	YLR079W	P40 inhibitor of Cdc28p-Clb5 protein kinase complex (31.45/50)
M223 G3	YLR082C	Smc4 protein member of SMC family (43.25/55)
M222 B6	YLR083C	integral membrane protein\ p24a protein (73.40/90)
M222 B4	YLR089C	(65.25/65)
M222 B4	YLR089C	(65.25/65)
M81 G5	YLR090W	Homolog of E. coli DnaJ closely related to Ydj1p (50.6/60)

M81 H6	YLR091W	(32.34/40)
M81 H6	YLR091W	(32.34/40)
M222 B8	YLR093C	(27.64/39)
M223 H2	YLR097C	(37.87/52)
M81 H5	YLR098C	DNA binding activator (71.31/75)
M222 D6	YLR099C	(43.47/48)
M82 C8	YLR100W	(38.38/?)
M82 C8	YLR100W	(38.38/?)
M81 A11	YLR102C	(29.28/45)
M82 F1	YLR103C	omosomal DNA replication initiation protein (71.53/?)
M222 E6	YLR107W	(44.55/48)
M222 D8	YLR109W	(19.47/38)
M81 G4	YLR113W	mitogen-activated protein kinase (MAP kinase) (47.96/60)
M81 A6	YLR114C	(84.07/100)
M81 A6	YLR114C	(84.07/100)
M223 D1	YLR119W	suppressor of mal-1 mutation (23.54/33)
M222 D7	YLR124W	(12.65/16)
M222 F8	YLR125W	(15.07/40)
M82 A2	YLR127C	APC (anaphase promoting complex) component (93.86/94)
M82 D7	YLR131C	activator of CUP1 expression (84.73/40)
M222 E7	YLR132C	(31.93/40)
M221 A3	YLR137W	(40.48/52)
M84 C6	YLR139C	(70.76/70)
M86 G9	YLR141W	Upstream activation factor subunit (40.04/55)
M221 E6	YLR142W	proline oxidase (52.47/60)
M84 C2	YLR144C	Identified as an activity necessary for actin polymerization in permeabilized cells (85.72/90)
M221 F6	YLR150W	(30.14/42)
M255 H6	YLR151C	(37.43/52)
M84 G3	YLR153C	acetyl-coenzyme A synthetase (75.16/75)
M221 G4	YLR155C	nitrogen catabolite-regulated cell-wall L-asparaginase II (39.85/50)

M221 A2	YLR160C	nitrogen catabolite-regulated cell-wall L-asparaginase II (39.85/50)
M84 A8	YLR164W	(18.59/19)
M221 B1	YLR167W	ubiquitin (16.83/16)
M221 B2	YLR168C	(25.33/35)
M86 G8	YLR172C	S-adenosylmethionine (AdoMet)-dependent methyltransferase of diphthamide biosynthesis (33.03/40)
M224 F1	YLR175W	major low affinity 55 kDa Centromere/microtubule binding protein (53.24/60)
M221 C2	YLR176C	(89.24/96)
M86 H5	YLR178C	suppressor of cdc25 (24.12/38)
M221 H4	YLR179C	(22.14/33)
M221 F5	YLR180W	S-adenosylmethionine synthetase (42.13/48)
M221 E4	YLR186W	(27.83/36)
M84 A7	YLR187W	(112.97/114)
M84 D8	YLR188W	ATP-binding cassette (ABC) transporter family member (76.56/76)
M84 H9	YLR189C	(131.81/?)
M84 D11	YLR190W	(54.12/70)
M84 G1	YLR191W	Peroxisomal membrane protein that contains Src homology 3 (SH3) domain (42.57/45)
M221 F3	YLR193C	(19.38/30)
M84 B7	YLR195C	N-myristoyl transferase (50.08/32)
M84 A10	YLR197W	homology to microtubule binding proteins and to X90565_5.cds (55.55/55)
M221 D1	YLR199C	(24.23/36)
M221 E2	YLR200W	Polypeptide 6 of a Yeast Non-native Actin Binding Complex homolog of a component of the bovine NABC complex (12.65/18)

M84 D4	YLR201C	(28.63/40)
M84 C7	YLR203C	Protein involved in maturation of COX1 and COB mRNA (47.99/48)
M224 H9	YLR206W	(67.54/76)
M86 F3	YLR208W	cytoplasmic protein involved in release of transport vesicles from the ER (32.78/34)
M84 E4	YLR209C	(34.24/35)
M84 D7	YLR211C	(15.43/25)
M224 H8	YLR213C	(46.45/54)
M221 E1	YLR215C	(39.63/40)
M86 G3	YLR216C	a cyclophilin related to the mammalian CyP-40\ physically interacts with RPD3 gene product (40.84/48)
M84 A6	YLR218C	(16.53/17)
M84 D10	YLR221C	(24.23/45)
M84 D3	YLR224W	(40.7/40)
M84 F7	YLR227C	(54.26/12)
M85 D4	YLR243W	(30.03/40)
M225 B2	YLR248W	Serine/threonine protein kinase (67.21/100)
M226 D8	YLR254C	(20.82/34)
M85 C1	YLR255C	(12.90/20)
M83 H2	YLR257W	(35.42/?)
M83 B4	YLR258W	Glycogen synthase (UDP-glucose--starch glucosyltransferase) (77.66/78)
M85 F4	YLR259C	heat shock protein 60\ chaperonin protein (62.95/65)
M274 E6	YLR260W	(75.68/78)
M85 C7	YLR261C	Ras-like GTP binding protein (11.91/20)
M85 G2	YLR265C	(37.65/37)
M85 G4	YLR267W	(62.81/64)
M85 B6	YLR268W	Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles (23.65/33)
M226 E8	YLR270W	(38.61/48)
M85 E1	YLR271W	(30.35/40)

M83 B3	YLR273C	Protein similar to Gac1p a putative type I protein phosphatase targeting subunit (71.31/45)
M85 C6	YLR276C	(65.47/70)
M85 F1	YLR279W	(14.3/20)
M85 C2	YLR280C	(12.79/20)
M225 E5	YLR283W	(34.65/35)
M85 D6	YLR284C	(30.83/37)
M85 A9	YLR286C	Endochitinase (61.85/66)
M225 F1	YLR287C	(39.08/50)
M265 F6	YLR288C	involved in checkpoint control and DNA repair (52.27/60)
M225 F5	YLR290C	(30.50/36)
M225 F6	YLR291C	negative regulator of GCN4 expression (41.94/56)
M226 F7	YLR300W	Exo-1 3-beta-glucanase (49.49/49)
M83 D2	YLR303W	(48.95/?)
M225 G6	YLR307W	(33.22/51)
M225 A6	YLR314C	Component of 10 nm filaments of mother-bud neck (57.23/80)
M85 B8	YLR316C	(17.96/28)
M85 B4	YLR321C	(46.89/60)
M226 A7	YLR323C	(28.52/38)
M225 D8	YLR324W	(57.64/98)
M88 F8	YLR332W	Protein required for mating (41.47/55)
M88 F3	YLR336C	(98.92/98)
M88 E7	YLR339C	(20.26/25)
M88 G8	YLR340W	60S ribosomal protein P0 (L10E). (34.43/36)
M88 A5	YLR345W	(56.1/64)
M88 D10	YLR349W	(18.59/50)
M228 C1	YLR350W	(23.87/33)
M88 F2	YLR351C	(32.04/38)
M88 B5	YLR353W	(66.44/80)
M88 E6	YLR354C	Transaldolase enzyme in the pentose phosphate pathway (36.88/45)
M228 E2	YLR359W	Adenylosuccinate Lyase (53.13/68)
M88 C5	YLR361C	(63.61/75)
M88 H7	YLR363C	(24.01/34)
M230 H3	YLR369W	(72.48/64)

M88 E5	YLR377C	fructose-1 6-bisphosphatase (38.31/45)
M333 E4	YLR396C	(76.04/78)
M230 D7	YLR412W	(30.35/40)
M89 A2	YLR423C	(45.90/50)
M89 D5	YLR426W	152-1052 (35.97/36)
M89 B2	YLR431C	(49.86/55)
M89 A3	YLR432W	(57.64/57)
M231 E2	YLR433C	Calcineurin subunit A\ type 2B protein serine/threonine phosphatase catalytic subunit A1\ cytoplasmic (60.86/61)
M89 G6	YLR435W	(27.5/36)
M89 E8	YLR437C	(14.66/14)
M89 A1	YLR438W	ornithine aminotransferase (46.75/46)
M229 H1	YLR439W	Mitochondrial 60S ribosomal protein L4 (35.2/45)
M89 C4	YLR441C	Ribosomal protein analogous to rat S3A (28.08/38)
M231 B1	YLR446W	(47.74/50)
M89 D4	YLR449W	(43.23/45)
M229 B2	YLR455W	(33.55/45)
M89 D3	YLR456W	(22.55/22)
M229 H2	YLR457C	(35.12/55)
M229 A6	YLR460C	(41.49/50)
M89 H8	YLR461W	member of the seripauperin protein\gene family (see Gene_class PAU) (13.31/13)
M231 C1	YLR462W	(22.33/34)
M89 E3	YLR464W	793-930 (23.87/23)
M231 C2	YML004C	lactoylglutathione lyase (glyoxalase I) (35.89/48)
M89 F3	YML005W	(50.93/50)
M89 F4	YML006C	(85.27/100)
M231 B4	YML007W	jun-like transcription factor (71.61/80)

M89 C7	YML008C	S-adenosylmethionine: delta 24-methyltransferase (42.26/50)	M90 F5	YML065 W	120-kDa (largest) subunit of origin recognition complex (ORC)\ shows homology to Cdc6p Cdc18p and Sir3p and to proteins from K. lactis S. pombe and humans (100.65/100)
M89 G3	YML011C	(19.50/20)	M90 C1	YML069 W	Binds to catalytic subunit of DNA polymerase alpha (Pol1p) (60.83/65)
M231 C3	YML012 W	Component of the COPII coat of certain ER-derived vesicles (23.32/32)	M90 E2	YML070 W	(64.45/64)
M231 H5	YML014 W	(30.8/38)	M90 F2	YML078 W	cyclophilin-3 (cyclosporin-sensitive proline rotamase-3) (20.13/20)
M89 E1	YML016C	serine-threonine phosphatase Z (76.25/76)	M227 A4	YML079 W	(22.22/33)
M89 D6	YML028 W	Thiol-specific antioxidant (21.67/32)	M227 B5	YML080 W	(46.64/55)
M231 D1	YML032C	(55.47/63)	M92 E1	YML085C	142-1460 alpha-tubulin (49.38/65)
M89 B5	YML034 W	(72.37/72)	M333 H4	YML095C	(23.13/34)
M231 E1	YML038C	(48.65/49)	M227 A7	YML098 W	TFIID subunit (18.48/33)
M89 B4	YML040 W	(48.51/55)	M90 B4	YML101C	(12.90/20)
M89 C5	YML041C	(30.83/40)	M92 G5	YML102 W	p60 subunit of the yeast omatin Assembly Factor-I (CAF-I) (51.59/55)
M229 F4	YML042 W	Carnitine O-acetyltransferase peroxisomal and mitochondrial (73.81/90)	M90 B6	YML110C	(33.80/40)
M231 A7	YML046 W	RNA splicing factor associated with U1 snRNP (69.3/83)	M90 B9	YML113 W	datin an oligo(dA).oligo(dT)-binding protein (27.49/30)
M92 B2	YML048 W	ExtraCellular Mutant (44.44/50)	M90 G1	YML114C	(56.13/60)
M90 D5	YML050 W	(34.32/40)	M92 B3	YML115C	Vanadate resistance protein (58.88/64)
M227 F7	YML053C	(23.45/36)	M202 B6	YML128C	(56.46/64)
M90 A1	YML054C	Cytochrome b2 [L--lactate cytochrome-c oxidoreductase] (65.04/65)	M92 A7	YMR002 W	(17.37/28)
M90 C2	YML055 W	(19.69/20)	M91 A1	YMR004 W	Protein required for sorting proteins to the vacuole (56.32/48)
M92 C7	YML060 W	43-kDa 8-oxo-guanine DNA glycosylase (41.47/50)	M233 A7	YMR009 W	(19.8/33)
M90 B1	YML061C	5' to 3' DNA helicase (94.52/95)	M91 C3	YMR014 W	(57.2/57)
M227 D2	YML062C	(43.25/64)			
M90 H4	YML064C	(26.98/27)			

M310 A6	YMR015C	cytochrome P450 involved in C-22 denaturation of the ergosterol side-chain (59.21/59)
M234 E7	YMR017 W	DBF2 Interacting Protein\ SNAP 25 homolog (43.78/46)
M91 B1	YMR020 W	(55.99/50)
M93 C2	YMR021C	metal-binding transcriptional activator (45.90/55)
M91 D3	YMR022 W	ubiquitin conjugating enzyme (18.36/32)
M234 D6	YMR024 W	(43.01/43)
M91 B5	YMR025 W	(32.56/40)
M234 B4	YMR030 W	(41.47/50)
M93 C1	YMR035 W	Inner membrane protease (mitochondrial protein) (19.58/32)
M234 H2	YMR036C	(60.97/64)
M234 C4	YMR037C	zinc finger protein (77.47/100)
M233 C5	YMR038C	(27.42/33)
M234 H8	YMR041C	(36.88/48)
M233 B10	YMR042 W	Regulator of arginine-responsive genes with ARG81 and ARG82 (19.58/34)
M93 D1	YMR043 W	putative transcriptional activator of alpha-specific genes (31.57/40)
M234 A3	YMR044 W	(52.46/98)
M93 G4	YMR046C	(48.43/60)
M91 E5	YMR048 W	(34.98/35)
M91 E1	YMR051C	(48.43/48)
M93 B6	YMR055C	(33.69/40)
M91 F1	YMR058 W	multicopper oxidase (70.07/60)
M234 A8	YMR063 W	(26.4/33)
M234 F10	YMR065 W	(55.55/64)
M234 H1	YMR066 W	(98.89/100)

M234 D3	YMR067C	(45.79/45)
M234 F4	YMR068 W	(46.97/50)
M233 G5	YMR069 W	(31.46/35)
M234 A7	YMR070 W	unknown function\ 2 Cys2-His2 zinc fingers at c-terminus glutamine and asparagine rich. (54.01/54)
M234 B8	YMR071C	(18.40/18)
M93 C8	YMR073C	(22.14/30)
M234 A2	YMR074C	(15.98/25)
M234 G4	YMR075 W	(75.45/80)
M91 F4	YMR077C	(24.34/32)
M303 E4	YMR079 W	166-1071 phosphatidylinositol transfer protein (33.55/35)
M255 D7	YMR080C	putative helicase (106.84/100)
M93 H1	YMR081C	(37.21/50)
M234 F9	YMR086 W	(105.71/115)
M234 C2	YMR088C	(61.85/64)
M93 C3	YMR089C	mitochondrial membrane ATPase of the CDC48VPAS1VSEC1 8 (AAA) family (90.78/98)
M234 A5	YMR090 W	(25.08/33)
M234 B6	YMR091C	(47.88/64)
M234 C7	YMR092C	Protein localizes to actin cortical patches. Probable binding site on actin lies on front surface of subdomain 3 and 4 (67.68/75)
M91 B6	YMR093 W	(56.54/56)
M242 A1	YMR096 W	Snooze: stationary phase-induced gene family (32.78/46)
M242 C2	YMR097C	(40.40/44)
M242 A3	YMR098C	(67.45/70)
M241 D4	YMR099C	(32.70/45)
M112 D6	YMR101C	(37.76/45)
M242 B7	YMR102C	(91.77/98)
M242 B1	YMR104C	protein kinase (74.50/98)

M242 D2	YMR105C	Phosphoglucomutase (62.62/62)
M107 D3	YMR106C	(69.22/90)
M242 D5	YMR108 W	acetolactate synthase (75.68/85)
M107 A8	YMR111C	(50.85/60)
M107 C1	YMR112C	(14.44/20)
M242 E2	YMR113 W	(47.08/48)
M112 E3	YMR114C	(40.51/55)
M112 F5	YMR116C	811-1233 (35.2/38)
M242 E8	YMR119 W	(68.75/68)
M112 F3	YMR121C	(22.47/38)
M107 G5	YMR123 W	(13.53/30)
M112 E6	YMR124 W	(103.84/110)
M242 E7	YMR125 W	transcriptional activator of glycolytic genes (94.49/94)
M242 E1	YMR127C	Protein involved in silencing HMR homologous to acetyltransferases (37.21/45)
M107 F4	YMR130 W	(33.33/40)
M242 F5	YMR131C	(56.24/75)
M107 E6	YMR132C	(22.91/30)
M242 F7	YMR133 W	Meiosis-specific recombination gene (47.96/47)
M242 G8	YMR134 W	(26.28/34)
M112 F2	YMR135 W-A	(19.58/32)
M112 G3	YMR136 W	(61.71/60)
M242 G5	YMR138 W	GTP-binding protein (21.12/31)
M107 F6	YMR139 W	protein kinase that phosphorylates the meiotic activator IME1 (40.81/50)
M242 G7	YMR140 W	(53.9/59)
M112 G1	YMR142C	407-1002 (22/38)
M107 H3	YMR144 W	(37.7/350)
M242 G6	YMR147 W	(24.64/35)

M107 F7	YMR148 W	(16.49/30)
M242 G3	YMR152 W	(40.36/52)
M242 H1	YMR157C	(28.08/32)
M242 H2	YMR158 W	(17.16/28)
M242 B5	YMR159C	Protein homologous to human Sin3 complex component SAP18 possible coiled-coil protein (16.53/26)
M242 H6	YMR161 W	Homologous to E coli dnaJ protein (24.75/34)
M242 A8	YMR170C	aldehyde dehydrogenase (NAD(P)+) likely cytosolic (55.69/62)
M242 A4	YMR173 W	flocculent specific protein\ contains >35 repeats of the amino acid sequence NNNDSYGS (47.41/55)
M242 D9	YMR177 W	(56.21/56)
M107 B2	YMR178 W	(30.25/36)
M242 B4	YMR180C	(35.23/49)
M242 A7	YMR183C	(32.48/46)
M242 B8	YMR184 W	(21.89/20)
M237 F4	YMR197C	Vti1p (23.90/34)
M104 C1	YMR201C	112-1200 (40.92/50)
M237 H2	YMR203 W	Mitochondrial outer membrane protein\ forms the outer membrane import channel (42.68/48)
M237 G4	YMR205C	phosphofructokinase beta subunit (105.52/125)
M237 C1	YMR209C	(50.30/55)
M104 C3	YMR211 W	(52.46/55)
M104 F4	YMR213 W	(65.01/75)
M96 F6	YMR214 W	dnaJ homolog (44.55/48)

M237 D1	YMR217 W	GMP synthase (57.86/57)
M104 A4	YMR220 W	48 kDa Phosphomevalonate kinase (49.72/62)
M104 E5	YMR222C	(24.56/40)
M310 B6	YMR224C	Protein required for double-strand break repair and meiotic recombination (76.25/80)
M104 E1	YMR225C	206-444 Mitochondrial ribosomal protein MRPL44 (YmL44) (10.89/14)
M104 D3	YMR227C	TFIID subunit (64.93/65)
M104 B4	YMR228 W	Mitochondrial RNA polymerase specificity factor (37.62/40)
M104 F1	YMR233 W	(24.97/25)
M96 H3	YMR235C	(44.80/55)
M237 B5	YMR237 W	(79.75/88)
M237 C7	YMR239C	Ribonuclease III (51.84/58)
M237 F1	YMR241 W	(34.65/35)
M237 A4	YMR244C -A	(11.47/16)
M238 C5	YMR244 W	(39.26/43)
M202 D6	YMR246 W	long-chain fatty acid--CoA ligase and synthetase 4 (76.45/98)
M202 C6	YMR250 W	(64.46/75)
M237 D2	YMR251 W	(40.47/48)
M237 B4	YMR252C	(14.77/18)
M104 B7	YMR255 W	(20.79/36)
M237 C4	YMR260C	Translation initiation factor eIFeIF--1A (16.86/21)
M237 E6	YMR262 W	(34.54/48)
M237 F7	YMR263 W	(22.22/30)

M104 D8	YMR264 W	(22.44/30)
M104 F3	YMR267 W	mitochondrial inorganic pyrophosphatase (34.21/38)
M237 F5	YMR269 W	(15.73/25)
M104 B6	YMR270C	Upstream activation factor subunit (40.28/55)
M104 D7	YMR271C	Orotate phosphoribosyltransferase 2 (25.00/40)
M237 E2	YMR274C	(34.68/38)
M237 E4	YMR276 W	ubiquitin-like protein (41.14/42)
M237 G6	YMR278 W	(68.53/75)
M239 A1	YMR281 W	(33.55/45)
M240 C2	YMR282C	basic hydrophilic 67.5 kDa protein (63.83/62)
M97 B3	YMR283C	Initiator methionine tRNA 2'-O-ribosyl phosphate transferase (56.46/56)
M97 E5	YMR285C	(56.68/55)
M274 D7	YMR288 W	(106.92/110)
M97 A1	YMR289 W	(41.35/40)
M97 H1	YMR290C	(55.58/55)
M239 D3	YMR290 W-A	(12.76/12)
M102 C4	YMR291 W	(64.57/70)
M97 G6	YMR293C	(51.07/55)
M102 A8	YMR294 W	Coiled-coil domain protein required for proper nuclear migration during mitosis (but not during conjugation) (41.14/55)
M239 C1	YMR295C	(21.70/33)

M240 D2	YMR296C	Probable component of serine palmitoyltransferase which catalyzes the first step in biosynthesis of long-chain sphingolipids (61.41/64)
M97 D3	YMR297 W	carboxypeptidase Y (58.63/58)
M239 D5	YMR299C	(34.45/45)
M240 D6	YMR300C	phosphoribosylpyrophosphate amidotransferase (56.13/53)
M239 D1	YMR303C	alcohol dehydrogenase II (38.31/52)
M97 E4	YMR305C	(42.82/60)
M97 D9	YMR309C	~100 kDa cytoplasmic protein (89.45/90)
M239 E1	YMR310C	(34.90/44)
M239 F2	YMR311C	Regulates activity of protein phosphatase 1 Glc7p which is involved in proper chromosome segregation (25.32/36)
M97 E3	YMR312 W	(30.14/40)
M239 E5	YMR314 W	alpha-type of subunit of 20S proteasome (25.85/31)
M97 A7	YMR315 W	(38.5/40)
M240 H8	YMR316C -B	(11.35/19)
M97 D1	YMR316 W	(37.07/37)
M239 H3	YMR318C	(39.63/52)
M239 F5	YMR320 W	(11.22/14)
M240 F6	YMR321C	(11.58/30)
M102 E8	YMR322C	(26.10/36)
M97 E9	YMR323 W	(48.18/50)
M240 G2	YMR325 W	(13.75/19)

M102 G4	YNL001 W	an ORF of unknown function located in a centromeric region duplicated between chromosomes III and XIV (DOM34 homologue on chromosome III is a pseudogene) (42.57/34)
M202 E6	YNL002C	(35.45/52)
M240 H7	YNL004W	hypothetical RNA-binding protein (47.3/48)
M239 B9	YNL005C	Mitochondrial ribosomal protein MRP7 (YmL2) (E. coli L27) (40.84/55)
M102 E1	YNL006W	(33.44/40)
M240 H2	YNL007C	sit4 suppressor dnaJ homolog (38.75/48)
M97 A5	YNL009W	peroxisomal NADP-dependent isocitrate dehydrogenase (46.31/46)
M97 C6	YNL010W	(26.62/30)
M239 A7	YNL011C	(48.87/52)
M97 G8	YNL012W	Transcription regulator (59.07/60)
M240 A3	YNL015W	Proteinase inhibitor I2B (PBI2) that inhibits protease Prb1p (yscB) (8.46/8)
M97 G3	YNL016W	poly(A)+ RNA-binding protein (49.94/50)
M97 D6	YNL018C	(67.45/67)
M239 B7	YNL019C	(31.37/39)
M240 B8	YNL020C	(70.21/71)
M240 H1	YNL022C	(53.93/50)
M240 A4	YNL024C	(27.09/36)
M97 B5	YNL025C	C-type cyclin (35.56/40)
M97 E6	YNL026W	(53.45/55)
M240 B7	YNL027W	(74.69/98)
M240 C8	YNL028W	(11.66/16)
M240 E9	YNL029C	Putative mannosyltransferase of the KRE2 family (57.45/57)
M240 A2	YNL030W	Histone H4 (HHF1 and HHF2 code for identical proteins) (11.44/14)

M102 G2	YNL031C	Histone H3 (HHT1 and HHT2 code for identical proteins) (14.99/20)
M97 A4	YNL032W	(31.02/55)
M240 A5	YNL033W	(31.45/35)
M240 B6	YNL034W	(67.43/71)
M239 C7	YNL035C	(42.82/49)
M239 D8	YNL036W	involved in secretion of proteins that lack classical secretory signal sequences (24.42/32)
M97 G9	YNL037C	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1 (39.63/40)
M240 B2	YNL038W	(23.43/20)
M97 A3	YNL039W	90 kd subunit of TFIIIB also called TFIIIB90 or B" or B"90 component (65.45/65)
M97 B4	YNL040W	(50.37/50)
M240 C6	YNL042W	(43.67/50)
M97 H7	YNL043C	(11.69/12)
M102 C9	YNL044W	(17.49/20)
M97 H9	YNL045W	(73.92/73)
M243 A1	YNL046W	(19.03/28)
M243 B2	YNL047C	(72.29/85)
M243 B8	YNL052W	Cytochrome-c oxidase chain Va (16.94/18)
M105 B8	YNL053W	(53.9/53)
M243 B1	YNL054W	(128.3/6130)
M105 H1	YNL055C	Outer mitochondrial membrane porin (voltage-dependent anion channel or VDAC) (31.26/31)
M105 G2	YNL056W	(21.78/36)
M243 B6	YNL058C	(34.79/48)
M243 C8	YNL061W	90-kDa protein located in nucleolus that is homologous to a human proliferation-associated nucleolar protein p120 (68.09/68)

M105 C8	YNL062C	RNA-binding (zeta) subunit of translation initiation factor 3 (eIF-3) (52.61/52)
M243 C1	YNL063W	(34.65/45)
M108 E2	YNL065W	(64.57/64)
M105 A4	YNL066W	Protein involved in the aging process (46.31/64)
M243 C6	YNL067W	ribosomal protein RPL9 (YL11) (21.12/36)
M105 A7	YNL069C	478-1046 Ribosomal protein (21.89/20)
M243 F9	YNL070W	translocase of the outer mito. membrane (6.71/7)
M105 C1	YNL071W	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex (53.13/50)
M247 A2	YNL072W	RNase H(35) a 35 kDa ribonuclease H (33.88/48)
M243 G3	YNL073W	mitochondrial lysine-tRNA synthetase (63.47/64)
M105 B4	YNL074C	(49.75/50)
M243 D6	YNL075W	(32.01/50)
M243 B7	YNL076W	negative regulator of Ras cAMP pathway (64.45/70)
M243 E8	YNL077W	(58.29/64)
M108 D8	YNL078W	(44.88/52)
M105 D1	YNL079C	tropomyosin I (21.92/32)
M247 B2	YNL080C	(40.39/47)
M243 E6	YNL083W	(54.45/64)
M247 C6	YNL084C	Protein necessary for internalization of alpha-factor receptor when bound to ligand (38.42/40)
M243 H9	YNL086W	(11.33/18)
M247 C3	YNL089C	(17.41/20)
M108 B4	YNL090W	GTP-binding protein of the rho subfamily of ras-like proteins (21.23/34)
M243 D7	YNL092W	(44.11/48)

M243 F8	YNL093W	rab5-like GTPase involved in vacuolar protein sorting and endocytosis (24.31/34)
M243 A10	YNL094W	(64.68/75)
M247 C2	YNL096C	490-918 (21.01/31)
M105 D3	YNL097C	(36.33/36)
M105 E4	YNL098C	Ras proto-oncogene homolog (35.45/48)
M105 D5	YNL099C	(26.21/32)
M243 E7	YNL100W	(25.85/34)
M243 H2	YNL104C	alpha-isopropylmalate synthase (2-Isopropylmalate Synthase) (68.12/68)
M247 E3	YNL105W	(15.73/17)
M243 G6	YNL107W	(24.97/36)
M108 E6	YNL108C	(29.73/40)
M243 C10	YNL110C	(24.23/31)
M108 F1	YNL111C	cytochrome b5 (13.23/20)
M243 D4	YNL113W	subunit common to RNA polymerases I (A) and III (C) (15.73/16)
M247 F4	YNL114C	(13.56/18)
M243 G7	YNL116W	(57.53/64)
M243 A9	YNL117W	carbon-catabolite sensitive malate synthase (61.05/64)
M105 H8	YNL118C	(106.73/100)
M243 H1	YNL119W	(54.34/68)
M243 A3	YNL120C	(17.74/25)
M243 F5	YNL122C	(12.68/20)
M247 H6	YNL124W	(54.23/90)
M255 F7	YNL128W	Similar to human tumor suppressor gene known as TEP1 MMAC1 and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases. (47.85/50)
M105 F3	YNL129W	(26.51/30)
M243 A7	YNL131W	Mitochondrial import receptor complex protein (16.83/30)
M243 C9	YNL133C	(19.06/20)

M247 A9	YNL134C	(41.49/50)
M243 A2	YNL135C	peptidylprolyl cis-trans isomerase (12.57/18)
M243 C3	YNL136W	(46.86/50)
M105 G4	YNL138W	70-kDa adenyl cyclase-associated protein (57.97/64)
M247 A7	YNL140C	(20.82/31)
M105 A8	YNL141W	(38.38/52)
M243 D10	YNL142W	Ammonia transport protein (55/55)
M103 E4	YNL148C	cofactor B (27./9748)
M103 C5	YNL149C	(14.22/28)
M244 F2	YNL152W	(45.1/57)
M244 H3	YNL153C	Polypeptide 4 of a Yeast Non-native Actin Binding Complex homolog of a component of the bovine NABC complex (14.22/26)
M244 A5	YNL154C	membrane-bound casein kinase I homolog (60.09/64)
M244 B6	YNL155W	(30.25/32)
M103 F4	YNL156C	(32.92/40)
M245 B8	YNL157W	(18.59/34)
M245 D9	YNL158W	(21.89/32)
M245 C1	YNL159C	(31.82/32)
M274 E7	YNL160W	Glycoprotein synthesized in response to nutrient limitation (39.05/42)
M244 A4	YNL161W	(83.37/95)
M110 E3	YNL163C	(122.13/?)
M245 A7	YNL164C	(38.64/49)
M103 D5	YNL165W	(44.77/52)
M245 E9	YNL166C	(49.31/49)
M245 G2	YNL168C	(28.52/38)
M244 B4	YNL169C	Phosphatidylserine Decarboxylase 1 (55.03/55)
M245 G5	YNL171C	(13.45/48)
M244 H8	YNL173C	(40.39/48)
M245 F9	YNL174W	(21.01/37)
M103 D1	YNL175C	(44.46/55)
M110 D2	YNL176C	(69.99/?)
M244 B5	YNL178W	Ribosomal protein RPS3 (rp13) (YS3) (Mammalian S3) (26.51/35)
M245 H5	YNL179C	(15.98/28)

M245 B7	YNL180C	(36.22/36)
M110 A6	YNL181W	(44.88/?)
M245 G9	YNL182C	(61.08/98)
M244 F1	YNL183C	protein kinase homolog (86.93/88)
M244 C4	YNL185C	(17.41/26)
M244 C5	YNL186W	(87.23/115)
M103 G3	YNL187W	(39.48/40)
M110 A5	YNL188W	Protein involved in spindle pole body duplication and karyogamy (47.74/70)
M110 B6	YNL189W	karyopherin alpha homolog of 60 kDa (59.73/59)
M245 H9	YNL190W	(22.55/95)
M244 G1	YNL191W	(39.48/44)
M245 C4	YNL193W	(61.49/65)
M103 B3	YNL194C	(33.14/42)
M103 H3	YNL195C	(26.76/36)
M110 B5	YNL196C	(32.81/40)
M24 F10	YNL198C	(11.03/16)
M245 G1	YNL199C	Activates transcription of glycolytic genes\ homologous to GCR1\ may function in complex with Gcr2p (58.77/50)
M103 B2	YNL200C	(27.09/38)
M103 C3	YNL202W	sporulation-specific protein (32.56/42)
M103 A4	YNL203C	(22.46/32)
M110 C5	YNL204C	sporulation-specific protein (33.03/33)
M244 G10	YNL206C	(50.08/60)
M110 F1	YNL207W	(46.86/46)
M244 D3	YNL208W	(22.55/33)
M244 F4	YNL209W	Heat shock protein of HSP70 family homolog of SSB1 (67.54/68)
M244 F5	YNL210W	mer2 splicing factor (29.81/32)
M110 B4	YNL211C	(9.496/9)
M110 D5	YNL212W	(86.13/86)
M110 E6	YNL213C	(23.57/30)
M110 G1	YNL215W	(35.31/64)
M245 D3	YNL216W	repressor activator protein (91.08/87)
M244 G4	YNL217W	(35.97/47)

M244 G5	YNL218W	(64.68/74)
M110 E5	YNL220W	adenylosuccinate synthetase (47.74/47)
M244 H10	YNL222W	(22.77/28)
M245 B2	YNL223W	(55.77/64)
M244 F3	YNL224C	(84.40/94)
M110 D4	YNL227C	(64.93/80)
M245 H7	YNL228W	(28.49/33)
M244 G9	YNL229C	transcriptional regulator putative glutathione transferase (38.97/48)
M245 E10	YNL230C	(41.72/41)
M110 A2	YNL231C	(38.64/?)
M103 D2	YNL232W	(32.23/40)
M110 D3	YNL234W	(46.97/?)
M265 A8	YNL236W	transcriptional silencer general repressor of diverse set of genes (107.35/107)
M103 F6	YNL238W	Ca ²⁺ -dependent serine protease (89.65/100)
M254 A1	YNL239W	Aminopeptidase of cysteine protease family (53.24/59)
M111 B2	YNL240C	(54.04/64)
M111 E3	YNL241C	Glucose-6-phosphate dehydrogenase (55.58/55)
M111 G5	YNL243W	transmembrane protein (106.59/106)
M254 E5	YNL244C	translation factor (11.91/25)
M254 H7	YNL246W	128-890 (29.15/30)
M111 C2	YNL248C	49-kDa alpha subunit of RNA polymerase A (45.68/55)
M249 C3	YNL249C	(59.65/58)
M111 D8	YNL253W	(46.53/55)
M254 A8	YNL254C	(44.14/53)
M249 B1	YNL255C	(16.86/21)
M109 G1	YNL256W	(95.25/95)
M254 E4	YNL259C	Antioxidant protein and metal homeostasis factor protects against oxygen toxicity (8.066/16)
M109 A6	YNL260C	(21.81/21)

M254 G6	YNL261W	Fifth largest subunit of origin recognition complex\ contains possible ATP-binding site (52.8/64)
M249 C1	YNL263C	(34.57/38)
M109 H1	YNL264C	(38.53/52)
M254 D2	YNL272C	Protein with coiled-coil domain essential for vesicular transport (83.52/97)
M254 F3	YNL274C	(38.53/42)
M254 F4	YNL275W	(63.47/63)
M254 H6	YNL277W	homoserine O-trans-acetylase (53.57/65)
M111 G9	YNL278W	(116.71/116)
M254 D1	YNL279W	(72.82/95)
M249 F3	YNL281W	(16.94/30)
M109 F3	YNL282W	(21.56/30)
M109 H4	YNL283C	(55.46/80)
M109 D6	YNL284C	(35.45/50)
M249 G7	YNL285W	(13.64/27)
M111 H9	YNL286W	Cold sensitive U2 snRNA Supressor (31.46/42)
M111 A5	YNL290W	Subunit 3 of Replication Factor C\ homologous to human RFC 36 kDa subunit (37.51/45)
M109 A5	YNL291C	plasma membrane protein (60.31/98)
M111 A10	YNL294C	(58.66/64)
M249 E2	YNL296W	(11.55/14)
M109 H3	YNL298W	protein kinase (92.73/98)
M111 A9	YNL301C	545-993 Ribosomal protein rp28 (rat L18) (20.57/34)
M111 A3	YNL304W	(39.26/50)
M111 A4	YNL305C	(32.70/32)
M109 A4	YNL306W	(23.98/35)
M109 C5	YNL307C	43.1 kDa Serine/threonine/tyrosine protein kinase (41.38/50)
M109 E6	YNL308C	(65.04/65)
M254 D7	YNL309W	sin3 binding protein (50.6/57)
M111 C10	YNL310C	(22.58/34)

M111 B3	YNL312W	116-930 subunit 2 of replication factor RF-A\ 29% identical to the human p34 subunit of RF-A (30.14/34)
M249 E4	YNL314W	positive regulator of allophanate inducible genes (28.26/36)
M109 D5	YNL315C	(35.01/40)
M111 C9	YNL317W	(51.36/55)
M254 H2	YNL320W	(31.45/42)
M254 C4	YNL322C	Cell wall beta-glucan assembly (34.46/50)
M254 C5	YNL323W	(45.65/50)
M111 E10	YNL326C	(36.99/40)
M249 A3	YNL328C	(16.09/20)
M109 F5	YNL331C	(41.49/50)
M109 H6	YNL332W	(37.51/35)
M249 D8	YNL333W	Snooze: stationary phase-induced gene family (32.89/40)
M114 A1	YNL335W	(24.86/34)
M113 F6	YNR001C	citrate synthase. Nuclear encoded mitochondrial protein. (52.72/67)
M257 G8	YNR002C	Putative transmembrane protein (31.05/36)
M257 C10	YNR003C	34-kDa subunit of RNA polymerase III (C) (34.90/45)
M257 B1	YNR004W	(16.27/26)
M257 E2	YNR005C	(14.77/18)
M253 H3	YNR006W	hydrophilic protein\ has cysteine rich putative zinc finger essential for function (68.53/100)
M114 C4	YNR007C	(34.13/45)
M253 B6	YNR008W	(72.82/90)
M253 D7	YNR009W	(27.5/38)
M257 H8	YNR010W	Protein required for accurate mitotic chromosome segregation (16.5/25)
M257 C1	YNR012W	Uridine kinase (55.22/55)
M113 F3	YNR014W	(23.43/45)

M253 C5	YNR015W	Suppressor of Mitochondrial Mutation in the tRNA ^{asp} gene (42.45/47)
M257 G7	YNR017W	23 kDa mitochondrial inner membrane protein (24.53/32)
M114 E7	YNR018W	(24.75/38)
M257 G2	YNR021W	(44.55/47)
M114 D4	YNR023W	73 kDa subunit of the SWIVSNF transcription activation complex (62.47/70)
M253 C6	YNR024W	(20.57/35)
M114 F7	YNR026C	integral membrane protein involved in protein transport to the Golgi (51.84/64)
M253 A10	YNR027W	(34.98/48)
M114 D1	YNR028W	(33.99/40)
M253 C4	YNR030W	ExtraCellular Mutant (60.72/70)
M114 D5	YNR032W	(40.59/48)
M257 A8	YNR033W	para-aminobenzoate synthase PABA synthase (86.68/98)
M114 G7	YNR034W	(35.42/40)
M114 B9	YNR035C	Arp Complex Subunit (37.65/45)
M114 E1	YNR036C	(16.86/30)
M113 H5	YNR040W	(28.37/50)
M253 G7	YNR041C	para hydroxybenzoate: polyprenyl transferase (40.95/41)
M253 A9	YNR042W	(15.73/30)
M257 G10	YNR043W	mevalonate pyrophosphate decarboxylase (43.67/49)
M253 E4	YNR046W	(14.96/20)
M253 F6	YNR048W	(43.44/60)
M113 B7	YNR049C	Multicopy Suppressor of sec1 (23.13/20)
M114 A8	YNR050C	Saccharopine dehydrogenase (NADP+ L-glutamate forming) (saccharopine reductase) (EC 1.5.1.10) (49.09/55)

M253 D10	YNR051C	(56.68/67)
M114 F1	YNR052C	Putative transcription factor (47.66/55)
M253 F4	YNR054C	(34.79/50)
M113 C7	YNR057C	(26.10/26)
M114 B8	YNR058W	7 8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase (52.91/55)
M253 E10	YNR059W	(63.91/64)
M253 C3	YNR061C	(24.12/38)
M113 B6	YNR064C	(31.93/64)
M257 G9	YNR066C	(47.99/50)
M253 A2	YNR068C	(29.95/32)
M257 C3	YNR069C	(53.82/60)
M114 H4	YNR071C	(37.65/45)
M113 E7	YNR073C	(55.35/64)
M257 B11	YNR075W	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p Ybr302p Cos3p Cos1p Cos4p Cos8p Cos6p Cos9p (41.35/47)
M113 C4	YOL001W	negative transcriptional regulator (32.34/50)
M257 C7	YOL003C	(41.61/45)
M253 E9	YOL005C	RNA polymerase II subunit (13.23/17)
M257 E3	YOL008W	(22.88/32)
M257 A5	YOL009C	Component of Mitochondrial Inheritance located in outer mitochondrial membrane (29.84/40)
M113 F7	YOL012C	Histone-related protein that can suppress histone H4 point mutation (14.77/25)
M257 B10	YOL013C	(60.64/64)
M116 B2	YOL016C	calmodulin dependent protein kinase (49.20/55)
M258 B1	YOL023W	mitochondrial initiation factor 2 (74.47/84)

M258 E3	YOL025W	Affects longevity (72.71/80)
M258 G4	YOL026C	(12.46/18)
M258 G6	YOL028C	(26.98/38)
M117 A7	YOL029C	(22.14/32)
M258 D2	YOL032W	(27.17/34)
M258 F3	YOL033W	Mitochondrial glutamyl-tRNA synthetase (59.07/69)
M258 A8	YOL037C	(12.90/34)
M258 E2	YOL040C	Ribosomal protein RPS21 (rp52) (E. coli S19) (rat S15) (RIG protein) (15.65/22)
M258 H4	YOL042W	(40.04/48)
M258 G5	YOL043C	Endonuclease III-like glycosylase 2 (41.83/47)
M258 H8	YOL046C	(24.67/34)
M258 F2	YOL048C	(11.69/16)
M116 H8	YOL053W	(43.56/45)
M116 E1	YOL054W	(44.77/80)
M258 G2	YOL055C	(60.64/60)
M116 G3	YOL056W	phosphoglycerate mutase (33.44/38)
M258 B5	YOL057W	(78.32/85)
M259 H5	YOL058W	arginosuccinate synthetase (46.31/55)
M258 B7	YOL059W	Glycerol-3-phosphate dehydrogenase (NAD+) (48.51/54)
M116 F7	YOL060C	(77.69/77)
M258 B9	YOL061W	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase) (54.67/60)
M116 H3	YOL064C	Putative phosphatase gene involved in salt tolerance and methionine biogenesis\ halotolerance (39.30/45)
M258 C5	YOL065C	(42.37/48)
M117 C5	YOL066C	DRAP deaminase (65.04/ 70)

M116 A7	YOL067C	Transcription factor (bHLH) involved in interorganelle communication between mitochondria peroxisomes and nucleus (19.50/28)
M303 D5	YOL068C	(55.46/65)
M258 A3	YOL080C	(31.82/44)
M117 C4	YOL082W	(45.76/60)
M259 A6	YOL083W	(45.43/53)
M116 D9	YOL086C	Alcohol dehydrogenase (38.31/45)
M116 G2	YOL088C	(30.50/40)
M258 E7	YOL092W	(33.99/35)
M116 B8	YOL093W	(32.34/40)
M116 E9	YOL094C	Subunit 4 of Replication Factor C\ homologous to human RFC 40 kDa subunit (35.56/52)
M116 H2	YOL096C	3 4-dihydroxy-5-hexaprenylbenzoate methyltransferase (34.79/40)
M117 F3	YOL097C	(47.55/50)
M258 D6	YOL099C	(17.96/25)
M116 C8	YOL101C	(34.35/40)
M258 D3	YOL104C	(38.75/45)
M258 E6	YOL107W	(37.73/42)
M202 A7	YOL108C	Transcription factor involved in activation of phospholipid synthetic genes (16.64/30)
M258 G8	YOL109W	(12.54/24)
M118 A1	YOL111C	(23.45/36)
M118 A4	YOL114C	(22.35/33)
M202 E7	YOL116W	43 kDa protein (42.13/64)
M282 G7	YOL118C	(11.35/16)
M278 D2	YOL120C	560-1008 Ribosomal protein rp28 (rat L18) (RP28A and RP28B code for identical proteins) (20.57/30)
M115 F5	YOL123W	Putative polyadenylated-RNA-binding protein located in nucleus\ similar to vertebrate hnRNP AVB protein family (58.85/70)

M282 G5	YOL124C	(47.66/50)
M115 H7	YOL125W	(52.47/64)
M278 E8	YOL126C	cytosolic malate dehydrogenase (46.56/60)
M278 E2	YOL128C	(41.38/49)
M278 A5	YOL131W	(11.99/16)
M115 A8	YOL133W	(13.42/20)
M282 A8	YOL134C	(14.22/14)
M282 B3	YOL137W	(54.78/64)
M118 D5	YOL139C	mRNA cap binding protein eIF-4E (23.46/27)
M282 B8	YOL142W	(26.51/34)
M278 E1	YOL143C	6 7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (18.62/30)
M278 C4	YOL146W	(26.07/34)
M118 E5	YOL147C	Peroxisomal biogenesis protein (peroxin) involved in peroxisome inheritance and peroxisomal proliferation (25.99/34)
M278 D6	YOL148C	putative transcription factor (66.47/75)
M115 F1	YOL151W	(37.73/45)
M278 D4	YOL154W	(27.5/37)
M278 D5	YOL155C	(106.4/0116)
M278 E7	YOL157C	(64.82/75)
M118 F1	YOL159C	(18.84/29)
M282 D2	YOL160W	(12.54/12)
M118 G3	YOL161C	(13.23/20)
M282 A4	YOL162W	(23.76/30)
M282 A5	YOL163W	(18.7/27)
M282 A7	YOL165C	(15.76/19)
M282 E8	YOL166C	(12.45/12)
M118 G1	YOR001W	Ribosomal RNA Processing (80.74/80)
M118 H3	YOR003W	subtilisin-like protease III (52.69/64)
M278 F4	YOR004W	(28.05/39)
M282 B5	YOR005C	ATP dependent DNA ligase (103.87/105)
M278 F6	YOR006C	(34.46/34)
M282 B7	YOR007C	(38.09/38)
M115 G9	YOR008C	(41.61/55)
M282 H1	YOR009W	(53.68/52)

M282 F2	YOR010C	Cold-shock induced protein of the Srp1p/Tip1p family of serine-alanine-rich proteins (27.64/35)
M282 C5	YOR013W	(17.37/27)
M278 G6	YOR014W	high copy suppressor of rox3 and a multicopy suppressor of hsp60-ts alleles (83.48/90)
M118 G9	YOR016C	(22.80/33)
M118 H5	YOR021C	(23.46/36)
M282 D7	YOR023C	(62.39/64)
M282 G8	YOR024W	(11.88/14)
M115 B2	YOR025W	Homolog of SIR2 (49.38/55)
M282 G2	YOR026W	(37.62/38)
M282 E3	YOR027W	heat shock protein (64.9/65)
M265 E8	YOR028C	(32.48/31)
M278 A7	YOR030W	ExtraCellular Mutant (68.2/80)
M118 A10	YOR032C	(47.77/47)
M115 C2	YOR033C	Protein that complements a drug-hypersensitive mutation (77.35/75)
M278 H4	YOR036W	integral membrane protein\ c-terminal TMD\ located in endosome (31.79/40)
M278 B6	YOR037W	cytochrome c mitochondrial import factor (44.55/49)
M282 F7	YOR039W	Casein kinase II beta' subunit (28.49/32)
M118 B10	YOR040W	Mitochondrial glyoxylase-II (31.46/45)
M279 A1	YOR041C	(15.76/12)
M119 H3	YOR043W	Protein involved in growth regulation (53.57/60)
M279 G3	YOR044W	(17.48/23)
M120 F7	YOR046C	RNA helicase (53.05/60)
M279 B1	YOR049C	(38.97/43)
M279 A2	YOR050C	(12.68/16)
M120 A4	YOR051C	(45.45/45)
M119 D5	YOR052C	(16.53/32)
M120 G7	YOR054C	(74.27/?)
M279 D7	YOR056C	(50.52/65)

M280 C2	YOR058C	encodes component of the spindle midzone (97.48/98)
M279 A4	YOR060C	(28.30/35)
M279 E5	YOR062C	(29.51/53)
M279 E6	YOR063W	ribosomal protein L3 (42.68/50)
M279 E7	YOR064C	(24.12/24)
M120 D1	YOR065W	Cytochrome c1 (34.1/7)
M119 E1	YOR073W	(65.01/75)
M279 B2	YOR074C	236-915 Thymidylate synthase (28.6/39)
M279 F5	YOR078W	(23.65/36)
M119 A3	YOR082C	(12.46/20)
M119 E4	YOR083W	(32.56/52)
M119 H5	YOR084W	(42.68/52)
M119 C7	YOR085W	34-kDa gamma subunit of oligosaccharyl transferase glycoprotein complex (38.61/45)
M119 B11	YOR088W	(53.13/40)
M120 G1	YOR089C	small GTP-binding protein\ geranylgeranylated\ geranylgeranylation required for membrane association\ also involved in endocytosis post vesicle internalization (23.13/33)
M279 E1	YOR089C	small GTP-binding protein\ geranylgeranylated\ geranylgeranylation required for membrane association\ also involved in endocytosis post vesicle internalization (23.13/33)
M119 F4	YOR091W	(44.22/55)
M119 A6	YOR092W	ExtraCellular Mutant (67.54/60)
M119 B10	YOR095C	(28.41/38)
M119 C11	YOR096W	546-974 (21.01/32)

M280 D3	YOR099W	type 2 membrane protein\ probable secretory protein (43.34/50)
M120 A6	YOR100C	(36.00/47)
M279 G5	YOR102W	16-kDa epsilon subunit of oligosaccharyltransferase complex\ 40% identical to vertebrate DAD1 protein (12.87/39)
M279 D2	YOR106W	member of the syntaxin family of proteins\ predicted C-terminal TMD (31.24/43)
M119 G4	YOR107W	(34.1/40)
M120 B6	YOR108W	(66.55/66)
M119 D10	YOR111W	(25.63/34)
M280 F2	YOR114W	(32.45/36)
M280 E3	YOR115C	(29.51/31)
M119 F7	YOR117W	(47.85/55)
M120 C10	YOR119C	(53.27/70)
M202 G7	YOR120W	Similar to mammalian aldo\keto reductases (34.43/50)
M120 C2	YOR121C	(11.14/11)
M119 A5	YOR123C	(51.07/75)
M120 H8	YOR126C	isoamyl acetate hydrolytic enzyme (26.21/50)
M280 H8	YOR128C	phosphoribosylamino-imidazole-carboxylase (62.84/62)
M279 F3	YOR131C	(24.01/30)
M119 H7	YOR133W	translation elongation factor 2 (EF-2) (92.73/98)
M119 C9	YOR134W	GTPase activating protein (GAP) (45.1/50)
M120 F11	YOR136W	NAD ⁺ -dependent isocitrate dehydrogenase (40.7/50)
M122 C2	YOR138C	(73.84/74)
M281 C7	YOR142W	(36.3/44)
M281 E8	YOR143C	Thiamin pyrophosphokinase (35.12/44)

M122 B1	YOR145C	(30.17/38)
M122 G10	YOR152C	(28.29/36)
M283 F2	YOR154W	(64.68/81)
M122 A4	YOR155C	(49.53/55)
M274 C8	YOR156C	Interacts with C-terminus of CDC12 (79.89/95)
M281 A6	YOR157C	putative proteasome subunit (28.74/36)
M122 E9	YOR159C	(10.47/18)
M121 C4	YOR163W	(20.79/20)
M281 A5	YOR164C	(34.45/40)
M122 C8	YOR166C	(50.41/34)
M122 A11	YOR168W	glutaminyt-tRNA synthetase (89.1/98)
M283 D1	YOR169C	(16.97/25)
M122 D8	YOR174W	(31.45/45)
M122 B11	YOR176W	ferrochelatase (protoheme ferrolyase) (43.34/48)
M122 C4	YOR179C	(20.71/30)
M281 C5	YOR180C	(29.84/35)
M122 A7	YOR181W	prolin rich protein (69.74/80)
M122 C11	YOR184W	phosphoserine transaminase (43.56/50)
M283 F1	YOR185C	GTP-binding protein (24.23/34)
M283 B3	YOR186W	(15.95/26)
M122 D4	YOR187W	(48.28/50)
M122 B7	YOR189W	(12.87/20)
M122 F8	YOR190W	Exo-1 3-beta-glucanase (49.06/52)
M122 B3	YOR194C	Transcription factor IIA large chain (31.49/42)
M121 E4	YOR195W	(90.42/90)
M281 D5	YOR196C	Involved in lipoic acid metabolism (45.57/55)
M281 F6	YOR197W	(49.94/60)
M121 A2	YOR201C	Ribose methyltransferase for mitochondrial 21S rRNA (45.35/55)

M122 A6	YOR204W	ATP-dependent RNA helicase of DEAD box family\ suppressor of a pre-mRNA splicing mutation prp8-1 (66.55/70)
M281 H6	YOR213C	(27.31/36)
M281 C9	YOR215C	(20.48/30)
M121 G11	YOR216C	(53.37/64)
M283 F3	YOR218C	(15.32/20)
M122 C6	YOR220W	(29.36/34)
M281 C8	YOR222W	(33.88/42)
M121 H11	YOR224C	16-kDa RNA polymerase subunit (common to polymerases I II and III) (16.09/20)
M281 D3	YOR226C	(17.29/18)
M122 A5	YOR227W	(137.27/138)
M121 G7	YOR229W	Transcriptional modulator (51.48/64)
M121 C9	YOR230W	Transcriptional modulator (48.28/65)
M121 A12	YOR232W	(25.29/33)
M123 A1	YOR233W	protein kinase (88.11/100)
M124 D4	YOR236W	dihydrofolate reductase (23.32/32)
M124 E8	YOR239W	(30.8/36)
M284 B8	YOR240W	(39.93/48)
M285 B1	YOR241W	(60.49/60)
M285 H2	YOR243C	(74.49/80)
M285 E4	YOR245C	(46.01/48)
M123 F6	YOR246C	(36.33/40)
M123 G7	YOR247W	(23.21/34)
M124 H9	YOR248W	(11.11/30)
M123 D2	YOR250C	(48.98/55)
M124 G3	YOR251C	(33.47/36)
M284 H3	YOR252W	(15.62/25)
M124 B6	YOR253W	(19.47/32)
M123 H7	YOR255W	(30.69/40)
M124 D1	YOR257W	Calcium-binding protein of spindle pole body (17.82/20)
M284 B2	YOR258W	(23.98/32)
M123 F3	YOR259C	ATPase\ component of the 26S proteasome cap subunit (48.10/55)

M124 G4	YOR260W	negative regulator in the general control of amino acid biosynthesis (63.69/70)
M124 C6	YOR261C	(37.21/38)
M124 F7	YOR262W	(38.38/40)
M123 C9	YOR264W	(47.41/55)
M284 E1	YOR265W	Binds to beta-tubulin and may participate in microtubule morphogenesis (11.77/14)
M284 C2	YOR266W	(46.64/50)
M285 G3	YOR268C	(14.55/30)
M124 D6	YOR269W	Required for viability in the absence of the kinesin-related Cin8p mitotic motor. (54.45/54)
M123 B8	YOR271C	(36.00/45)
M123 D9	YOR272W	microtubule-associated protein (50.71/60)
M284 D2	YOR274W	transfer RNA isopentenyl transferase (47.29/52)
M284 C4	YOR276W	mRNA cap-binding protein (eIF-4F) 20K subunit (17.82/30)
M124 G7	YOR278W	uroporphyrinogen III synthase (30.46/36)
M124 B9	YOR279C	(34.13/36)
M124 C10	YOR280C	(29.39/36)
M124 G1	YOR281C	(31.49/32)
M124 B5	YOR284W	(26.84/36)
M124 F6	YOR285W	(15.4/20)
M285 H5	YOR286W	(16.5/16)
M123 D8	YOR287C	(33.03/48)
M124 D10	YOR288C	Disulfide isomerase related protein (35.01/40)
M123 F1	YOR289W	(27.72/34)
M124 A8	YOR294W	(22.44/36)
M123 E8	YOR295W	(25.29/36)
M255 H8	YOR298W	(52.8/52)
M123 C6	YOR301W	(47.96/50)
M123 F8	YOR303W	Carbamoyl phosphate synthetase arginine specific (45.32/48)
M285 G7	YOR311C	(31.93/34)

M285 G1	YOR312C	415-932 60S ribosomal protein L18A (19.35/29)
M285 F2	YOR313C	(37.21/47)
M123 D7	YOR317W	long chain fatty acyl:CoA synthetase (77.11/80)
M124 F10	YOR319W	homolog of mammalian splicing factor/U2 snRNP protein (23.54/34)
M124 G5	YOR323C	gamma-glutamyl phosphate reductase (50.29/55)
M124 C7	YOR324C	(66.35/70)
M285 C6	YOR325W	(17.48/19)
M284 B9	YOR327C	vesicle-associated membrane protein (synaptobrevin) homolog (12.68/22)
M100 F1	YOR329C	(95.95/98)
M293 H2	YOR331C	27-kDa subunit of the vacuolar ATPase\ E subunit of V1 sector (20.48/21)
M100 F5	YOR335C	Cytoplasmic alanyl-tRNA synthetase gene (105.41/98)
M310 C7	YOR339C	(17.29/28)
M310 D7	YOR342C	(35.12/42)
M100 A1	YOR344C	33 kDa serine-rich protein (32.04/45)
M100 G2	YOR347C	(55.69/60)
M100 H5	YOR351C	kinase involved in meiotic chromosome pairing and recombination (54.70/60)
M100 B1	YOR352W	(37.84/45)
M100 H2	YOR355W	(57.53/64)
M100 E3	YOR356W	(69.52/69)
M100 D4	YOR357C	(17.85/25)
M100 H4	YOR358W	Component along with Hap2p and Hap3p of CCAAT-binding transcription factor (26.73/40)
M106 E6	YOR359W	(57.64/57)
M293 H6	YOR367W	(22.11/36)
M100 C1	YOR368W	DNA Damage checkpoint control (44.22/64)

M100 D2	YOR370C	Rab geranylgeranyl transferase (66.46/70)
M100 G3	YOR372C	(60.97/62)
M100 B5	YOR374W	(57.2/60)
M288 E7	YOR375C	NADP-specific glutamate dehydrogenase (49.97/55)
M100 D1	YOR376W	(13.53/20)
M100 A3	YOR379C	(12.45/16)
M100 H3	YOR380W	(60.17/60)
M100 H1	YOR385W	(32.01/40)
M100 B3	YOR387C	(22.69/30)
M100 C5	YOR390W	(41.46/41)
M100 C6	YOR391C	(26.10/32)
M293 E1	YOR392W	(16.38/20)
M100 A2	YOR393W	enolase homolog (48.28/55)
M100 C3	YPL001W	histone acetyltransferase (41.25/48)
M106 H5	YPL004C	(37.54/52)
M106 G6	YPL005W	(66.77/66)
M100 B2	YPL007C	(64.71/50)
M293 B2	YPL007C	(64.71/62)
M100 D3	YPL009C	(114.21/48)
M100 B4	YPL010W	Coatomer complex zeta chain (zeta-COP) of secretory pathway vesicles (20.9/32)
M288 F5	YPL011C	(38.86/52)
M100 E5	YPL012W	(135.29/135)
M100 C2	YPL015C	Homolog of SIR2 (39.30/45)
M100 C4	YPL026C	Serine/threonine protein kinase that suppresses the growth defect of snf3 mutants on low glucose (55.35/55)
M126 A1	YPL030W	(62.48/64)
M126 C2	YPL031C	120-1020 negative transcriptional regulator protein kinase homolog (33.66/38)
M126 F3	YPL032C	(90.78/90)
M286 D4	YPL033C	(30.94/40)
M286 E5	YPL034W	(18.36/31)
M127 G9	YPL037C	(17.30/25)
M127 B1	YPL038W	(19.58/32)

M126 G3	YPL040C	nuclear encoded mitochondrial isoleucyl-tRNA synthetase (110.35/110)
M287 F4	YPL042C	a cyclin(SSN8)-dependent serine/threonine protein kinase (61.08/54)
M127 E7	YPL043W	RNA recognition motif-containing protein (75.46/80)
M126 H3	YPL048W	Calcium and phospholipid binding protein homologous to translation elongation factor-1 gamma (EF-1 gamma) (45.76/45)
M126 D6	YPL050C	Protein required for complex glycosylation (43.48/45)
M286 G6	YPL051W	(21.89/30)
M126 G8	YPL052W	(22.22/30)
M126 A10	YPL053C	similar to KRE2 (49.09/50)
M126 C1	YPL054W	(33.22/38)
M127 B2	YPL055C	(36.55/42)
M287 B4	YPL057C	Multicopy suppressor of cls2-2\ also suppresses rvs161 mutations (42.05/42)
M286 H6	YPL059W	(16.61/16)
M287 D1	YPL062W	(14.85/26)
M126 F2	YPL063W	(52.47/55)
M126 B4	YPL064C	(33.14/40)
M126 C5	YPL065W	soluble hydrophilic protein involved in transport of precursors for soluble vacuolar hydrolases from the late endosome to the vacuole (26.73/32)
M126 A9	YPL068C	(32.36/38)
M126 B10	YPL069C	geranylgeranyl diphosphate synthase (36.88/38)
M126 E1	YPL070W	(67.43/67)
M126 G2	YPL071C	(17.29/20)
M286 G3	YPL072W	(55/60)
M126 F6	YPL074W	(83.05/83)

M126 C10	YPL077C	(26.4/332)
M126 F1	YPL078C	F(1)F(0)-ATPase complex delta subunit mitochondrial (26.87/30)
M286 F2	YPL079W	433-904 (17.71/27)
M287 G3	YPL080C	(11.91/12)
M126 E5	YPL081W	509-1095 (21.78/21)
M126 G1	YPL086C	(61.30/62)
M126 D4	YPL088W	(37.73/45)
M287 G5	YPL091W	Glutathione oxidoreductase (53.24/53)
M127 E10	YPL093W	(71.38/80)
M286 G1	YPL094C	membrane component of ER protein translocation apparatus (31.26/38)
M126 G5	YPL097W	Tyrosyl-tRNA synthetase (54.23/54)
M126 B8	YPL099C	(20.05/20)
M286 E8	YPL100W	(54.67/64)
M126 D10	YPL101W	(50.37/52)
M287 G1	YPL102C	(11.03/11)
M286 A3	YPL103C	(51.51/55)
M127 A7	YPL106C	Member of the 70-kDa heat-shock protein family (76.36/80)
M287 A6	YPL107W	(27.49/36)
M126 D9	YPL108W	(18.59/28)
M126 E10	YPL109C	(59.76/59)
M126 D3	YPL111W	arginase (36.74/40)
M126 H5	YPL113C	(43.59/45)
M126 E9	YPL116W	(76.78/76)
M287 H1	YPL118W	(37.95/51)
M126 E3	YPL119C	putative ATP-dependent RNA helicase\ Dead box protein (67.90/67)
M126 F4	YPL120W	(61.48/64)
M126 D8	YPL123C	(47.77/55)
M126 F9	YPL124W	Nuclear import protein (27.94/32)
M129 A2	YPL127C	histone H1 (28.41/38)
M130 E3	YPL128C	TTAGGG repeat binding factor (61.85/64)

M130 D4	YPL129W	115-840 (26.95/30)
M129 G6	YPL131W	Ribosomal protein RPL1 (YL3) (rat L5) (32.78/40)
M129 C8	YPL132W	Putative heme A biosynthetic enzyme involved in forming the formyl group at position 8 of the porphyrin ring (33.11/40)
M291 C8	YPL133C	(49.09/55)
M289 B1	YPL134C	(34.13/40)
M130 E2	YPL135W	(18.36/18)
M289 F5	YPL138C	(38.86/48)
M291 G5	YPL139C	Transcriptional modulator (50.63/60)
M255 D9	YPL141C	(95.28/98)
M129 C4	YPL145C	Homologous to human oxysterol-binding protein\ implicated in ergosterol biosynthesis and regulation of Golgi-derived transport vesicle biogenesis (47.77/55)
M130 F5	YPL146C	(50.08/55)
M129 E8	YPL148C	(19.50/30)
M129 A10	YPL149W	involved in autophagy (32.45/34)
M289 D1	YPL150W	(99.22/105)
M129 D2	YPL151C	(49.64/52)
M129 C3	YPL152W	(39.49/50)
M289 E4	YPL153C	(90.34/98)
M129 F8	YPL156C	(31.37/36)
M129 B10	YPL157W	(34.76/40)
M130 E1	YPL158C	(83.41/98)
M129 E2	YPL159C	(27.86/34)
M129 H5	YPL162C	(30.06/40)
M291 D7	YPL164C	(78.68/79)
M130 E9	YPL165C	(41.06/45)
M130 F1	YPL166W	(23.54/33)
M289 F3	YPL168W	(47.41/50)
M291 F3	YPL169C	(65.92/100)
M129 D7	YPL171C	NAD(P)H dehydrogenase (44.03/48)
M130 F9	YPL173W	(32.78/36)

M130 G1	YPL174C	Nuclear import protein (95.51/98)
M291 G3	YPL177C	Homeobox-domain containing protein (33.69/57)
M129 A6	YPL178W	(22.99/34)
M291 C6	YPL179W	protein phosphatase Q (60.5/63)
M130 G9	YPL181W	(55.77/50)
M291 B5	YPL186C	(33.47/57)
M130 D8	YPL188W	(45.65/52)
M289 H1	YPL190C	(88.35/100)
M130 B3	YPL191C	(39.63/49)
M129 A5	YPL193W	(42.02/52)
M129 C6	YPL194W	(67.43/70)
M130 E8	YPL196W	(30.14/34)
M130 C3	YPL199C	(26.43/38)
M129 B5	YPL201C	(50.74/55)
M130 D7	YPL203W	(41.91/50)
M130 F8	YPL204W	casein kinase I isoform (54.45/54)
M291 F1	YPL206C	(35.34/37)
M130 B4	YPL208W	(64.24/64)
M289 D5	YPL209C	Protein kinase (40.40/50)
M130 D6	YPL210C	(71.09/71)
M130 E7	YPL211W	(20.02/32)
M130 A10	YPL213W	(26.39/32)
M289 C2	YPL214C	TMP pyrophosphorylase hydroxyethylthiazole kinase (59.43/62)
M130 D3	YPL215W	(36.96/38)
M130 F7	YPL219W	(54.23/64)
M291 B8	YPL220W	homologue of the E- and Archebacterial L1 ribosomal protein of the 60S ribosomal subunit (23.98/33)
M129 H10	YPL221W	(87.34/70)
M292 A1	YPL222W	(75.79/76)
M132 G1	YPL223C	(18.51/28)
M132 A3	YPL225W	(16.27/20)
M132 G5	YPL228W	(60.5/68)
M133 A1	YPL230W	(43.12/55)
M132 E2	YPL232W	(32.01/45)
M292 B3	YPL233W	(23.87/33)
M292 H3	YPL234C	17-kDa subunit C of vacuolar membrane H(+)-ATPase (18.07/32)

M132 H5	YPL236C	(40.07/45)
M132 A7	YPL237W	beta subunit of translation initiation factor eIF-2 (31.46/34)
M133 B2	YPL239W	(22.11/32)
M290 A3	YPL240C	heat shock protein (78.02/98)
M292 C3	YPL241C	106-887 involvement in microtubule function (29.59/33)
M290 D5	YPL243W	Signal recognition particle subunit (66/70)
M292 F5	YPL244C	(37.32/37)
M133 C8	YPL245W	(50.0/555)
M292 C1	YPL246C	(28.85/29)
M133 C2	YPL247C	(57.56/60)
M132 B6	YPL252C	(18.95/30)
M133 D8	YPL253C	(71.20/71)
M132 D1	YPL254W	(53.79/55)
M292 D3	YPL257W	(21.34/33)
M255 E9	YPL258C	(60.64/60)
M290 F5	YPL259C	medium subunit of the clathrin-associated protein complex (52.38/64)
M133 B7	YPL260W	(60.72/70)
M132 E1	YPL262W	mitochondrial and cytoplasmic fumarase (fumarate hydratase) (53.79/53)
M133 E2	YPL263C	(71.64/75)
M132 C5	YPL267W	(23.1/34)
M132 C7	YPL269W	(70.95/70)
M290 C3	YPL272C	(56.90/64)
M132 F3	YPL273W	(35.86/36)
M290 H5	YPL275W	(26.07/36)
M292 A6	YPL276W	(16.06/31)
M133 F8	YPL277C	(53.60/60)
M290 C1	YPL278C	(11.03/20)
M290 D3	YPL280W	(26.28/34)
M292 F3	YPL281C	Enolase-related subtelomeric sequence (ERR1 and ERR2 code for identical proteins) (48.10/41)
M133 B5	YPL282C	(18.07/32)
M290 F6	YPR001W	Citrate synthase (53.57/54)

M132 G2	YPR005C	polar 32k Da cytoplasmic protein (32.47/38)	M134 G2	YPR060C	chorismate mutase (28.29/34)
M132 D4	YPR007C	(74.83/80)	M294 G3	YPR061C	(33.14/43)
M133 C6	YPR008W	(76.45/76)	M294 B5	YPR062W	cytosine deaminase (17.49/27)
M133 G1	YPR011C	(35.89/50)	M131 B6	YPR063C	128-509 (15.51/30)
M290 E3	YPR013C	(34.90/34)	M295 E9	YPR065W	site-specific DNA binding protein repressor (40.59/49)
M292 G3	YPR014C	(12.02/56)	M134 E11	YPR066W	(33/36)
M132 E4	YPR015C	(27.20/34)	M131 C1	YPR067W	(20/4630)
M132 E5	YPR016C	(26.98/32)	M294 D2	YPR068C	Protein with similarity to Hda1p Rpd3p Hos2p and Hos3p (51.73/60)
M290 H6	YPR017C	GDP dissociation factor for Sec4p (15.76/25)	M131 D3	YPR069C	putrescine aminopropyltransferase (spermidine synthase) (32.36/34)
M132 B2	YPR020W	(12.76/12)	M134 G5	YPR070W	(62.47/64)
M133 E5	YPR023C	(44.14/55)	M134 C7	YPR071W	(23.32/32)
M132 F5	YPR024W	Mitochondrial protein of the CDC48VPAS1VSEC1 8 family of ATPases (82.38/82)	M131 F8	YPR073C	18-kDa phosphotyrosine phosphatase of unknown function (17.74/25)
M133 G7	YPR025C	cyclin (43.36/50)	M294 D10	YPR074C	Transketolase 1 (74.83/85)
M290 E1	YPR027C	(30.50/30)	M134 F1	YPR075C	(39.63/48)
M132 C2	YPR028W	185-676 (19.91/20)	M131 C6	YPR079W	(42.02/42)
M133 H7	YPR033C	cytoplasmic and mitochondrial histidine tRNA synthetases (60.09/60)	M134 H8	YPR080W	translational elongation factor EF-1 alpha (50.49/50)
M294 A1	YPR035W	glutamine synthetase (40.81/47)	M295 G9	YPR081C	(68.01/68)
M134 E2	YPR036W	54-kDa vacuolar H(+) ATPase subunit of V1 sector (52.69/52)	M134 G11	YPR082C	(15.76/25)
M134 H3	YPR037C	(21.59/25)	M294 F2	YPR084W	(50.37/58)
M295 A8	YPR040W	(39.37/50)	M131 A5	YPR086W	transcription factor TFIIB homolog (38.06/48)
M295 C9	YPR041W	Translation initiation factor eIF-5 (44.66/52)	M295 C7	YPR087W	(11.77/14)
M131 A7	YPR048W	(68.64/68)	M134 H1	YPR091C	(84.73/84)
M134 C1	YPR051W	N-acetyltransferase (19.47/30)	M294 G2	YPR092W	(11.22/16)
M294 A5	YPR054W	Sporulation-specific MAP kinase required for completion of sporulation (42.79/55)	M134 G4	YPR093C	(34.13/36)
M134 A10	YPR057W	Protein involved in snRNP biogenesis (37.62/45)	M131 D1	YPR099C	(13.01/13)
M134 D11	YPR058W	putative mitochondrial carrier protein (33.88/40)	M294 D4	YPR101W	(19.46/34)
			M131 C5	YPR102C	(19.27/20)

M134 C9	YPR104C	Protein with a domain similar to the fork head DNA-binding domain found in the developmental fork head protein of <i>Drosophila melanogaster</i> and in the HNF-3 family of hepatocyte mammalian transcription (102.99/102)
M131 E1	YPR107C	Yeast 30kDa Homologue (22.91/33)
M295 E3	YPR108W	(47.3/54)
M131 D5	YPR110C	RNA polymerase III (C) subunit (36.88/45)
M131 A8	YPR112C	(97.60/98)
M134 C2	YPR115W	(119.24/119)
M294 B3	YPR116W	(30.58/42)
M131 E5	YPR118W	(45.32/50)
M131 B8	YPR120C	(47.88/47)
M301 C4	YPR121W	(63.03/66)
M295 D2	YPR123C	(15.87/25)
M295 G3	YPR124W	High affinity copper transporter into the cell probable integral membrane protein (44.77/37)
M131 C4	YPR125W	(50.05/55)
M131 G6	YPR127W	(38.06/45)
M294 F8	YPR128C	(36.11/40)
M134 B11	YPR129W	multicopy suppressor of clathrin deficiency (38.5/50)
M263 A1	YPR131C	(27.64/36)
M263 G2	YPR133C	(45.13/55)
M263 E3	YPR134W	Protein involved in splicing intron $\alpha 5$ of COX1 (29.59/34)
M263 C5	YPR136C	(18.73/31)
M263 B6	YPR137W	(63.14/80)
M264 F6	YPR138C	Ammonia permease of high capacity and low affinity (53.82/60)
M264 B1	YPR139C	(33.03/36)
M255 H9	YPR140W	(42.02/40)
M264 C4	YPR143W	(27.61/47)
M264 B6	YPR145W	asparagine synthetase (63.03/67)
M264 G6	YPR146C	(12.02/16)
M264 C1	YPR147C	(33.47/40)
M264 B2	YPR148C	(47.88/60)
M263 H2	YPR149W	involved in secretion of proteins that lack classical secretory signal sequences (19.14/25)
M263 E4	YPR151C	(22.69/32)
M263 E5	YPR152C	(51.28/60)
M263 A3	YPR157W	(51.48/64)
M263 H3	YPR158W	(27.83/42)
M264 D1	YPR163C	Translation initiation factor eIF-4B (47.99/50)
M263 B3	YPR165W	GTP-binding protein of the rho subfamily of ras-like proteins (23.1/30)
M263 A4	YPR166C	14 kDa mitochondrial ribosomal protein\ homologous to E. coli S14 protein (12.68/17)
M263 F4	YPR167C	3'phosphoadenylylsulfate reductase (28.74/36)
M263 D6	YPR169W	(56.65/62)
M263 C7	YPR170C	(12.24/18)
M263 C2	YPR172W	(22.11/33)
M263 C3	YPR173C	defective in vacuolar protein sorting (48.10/56)
M264 A4	YPR174C	(24.34/35)
M263 G4	YPR175W	DNA polymerase epsilon subunit B (76.23/76)
M264 F5	YPR176C	Geranylgeranyltransferase Type II beta subunit (35.78/39)
M264 D6	YPR177C	(13.56/17)
M263 D7	YPR178W	associated with the U4VU6 snRNP (51.36/55)
M264 D2	YPR180W	Along with Uba2p forms a heterodimeric activating enzyme for Smt3p (38.38/40)
M264 B4	YPR182W	Sm or Sm-like snRNP protein (9.57/10)

M264 H4	YPR183W	dolichol phosphate mannose synthase (29.48/36)
M263 E7	YPR186C	Transcription factor IIIA (47.22/51)
M264 E1	YPR187W	97-544 subunit common to RNA polymerases I II and III (17.26/29)
M263 E2	YPR188C	(17.96/30)
M263 A5	YPR191W	40 kDa ubiquinol cytochrome-c reductase core protein 2 (40.59/46)

M263 H5	YPR192W	(33.66/40)
M264 E6	YPR193C	(17.29/28)
M264 B5	YPR199C	(32.37/39)
M265 A10	YPR200C	(14.33/16)
M264 E7	YPR202W	168-865 (26.39/26)
M264 G1	YPR203W	(11.33/16)

Example 2 - High-throughput Expression of Human Gene Sequences

The following example illustrates the construction of a library of expressible
5 human gene sequences using the method of the invention. Primers were constructed
based on sequences of human genes available from GenBank.

Fetal human heart tissue was obtained from the International Institute for the
advancement of Medicine (IIAM). Poly A+ mRNA was isolated using the
FastTrack™ 2.0 Kit (Invitrogen, Carlsbad, CA) according to the manufacturer's
10 instructions. The mRNA was converted to first-strand cDNA using a cDNA Cycle®
Kit (Invitrogen) using the oligo dT primer provided and the protocols suggested. A
single cDNA synthesis reaction was split into 12 separate wells of a 96-well PCR
amplification plate, and PCR amplifications were performed using specific primer
sets, essentially as described above, with the exception that the ratio of Taq to Pfu was
15 50:1 in the initial amplification (final conc. 2 U Taq:0.04 U Pfu/well). Sequence
specific primers for each sequence being amplified were designed to start
amplification at the start codon (ATG) of each sequence and end at the stop codon. In
some cases, the primer design removed the stop codon from the DNA sequence,
allowing for generation of a fusion protein when inserted into suitable expression
20 vectors. Primers were synthesized using a Primerstation 960 (Intelligent Automation
Systems, Inc.) used according to the manufacturer's instructions and were designed
from sequences downloaded from Unigene and sent directly to the synthesizer.

Approximately 15 nMoles of each primer, having an average length of 25 basepairs (melting point between 60° - 64° C, was synthesized in a 96-well format. After synthesis, the primers were cleaved from the supports, deprotected and dried in the same 96-well format (see manufacturer's instructions).

- 5 The amplified gene sequences were purified and inserted into the pcDNA3.1/GS expression vector or pTYB2.2 expression vector (Invitrogen, Carlsbad, CA) essentially as described above. The expression vectors containing sequences verified to be in the correct orientation were transfected into CHO cells in 96-well deep-well blocks using the Pfx-6 PerFect Lipid system (Invitrogen, Cat #T930-16).
- 10 Cell lysates were made 48 hours after transfection, and the lysates were separated by SDS-PAGE and analyzed by Western blot according to standard protocols using an anti-V5 epitope tag Mab/horseradish peroxidase conjugate. Table 2 below lists the human proteins successfully expressed using this methodology. The ORFs identified as HP---- were expressed in pTYB2.2. All other ORFs were expressed in pDNA3.1.
- 15 Additional collections of human sequences were obtained from a variety of sources, including adult lung, heart and mammary tissue and fetal liver tissue. Sequences were inserted into several expression vectors having features suitable for different purposes, including pIND/GS, pRSET, pCRT7, pcDNA3.1/GS, and pBAD/Thio-V5-His (Invitrogen, Carlsbad, CA). Sequences obtained are listed in
- 20 Table 2 below.

Table 2 - Human ORFs

Plate Number	Accession Number	Description	Predicted Size	Actual Size
M235 C7	H-A06977	albumin	67.1	67.0kDa
E1	H-AB002391	Human mRNA for KIAA0393 gene, complete cds	68.09	68
H3	H-AB006969	Homo sapiens hGAA1 mRNA, complete cds	68.42	70
E2	H-AB007875	Homo sapiens KIAA0415 mRNA, complete cds	51.48	51
D1	H-AB007887	Homo sapiens KIAA0427 mRNA, complete cds	66.55	70

M421 D6	H-AB010710	Homo sapiens mRNA for lectin-like oxidized LDL receptor, complete cds	30.14	45.0kDa
G3	H-AD001528	Homo sapiens spermidine aminopropyltransferase mRNA, complete cds	40.37	40
B5	H-AE000659	Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the C	12.39	16
E2	H-AF004022	Homo sapiens protein kinase mRNA, complete cds	38.28	44
M428 C1	H-AF004231	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds	65.78	70.0kDa
A5	H-AF004327	Homo sapiens angiopoietin-2 mRNA, complete cds	54.67	60
C1	H-AF006501	Homo sapiens chromosome 22 cosmid clone c1155, RNA polymerase II subunit 14.4 kDa (POLRF) gene, complete cds	14.08	24
H4	H-AF008936	Homo sapiens syntaxin-16B mRNA, complete cds	35.75	47
H5	H-AF009243	Homo sapiens proline-rich Gla protein 2 (PRGP2) mRNA, complete cds	22.33	36
M462 D6	H-AF013249	Homo sapiens leukocyte-associated Ig-like receptor-1 (LAIR-1) mRNA, complete cds	31.68	40.0kDa
A1	H-AF013512	untitled	53.02	53
A3	H-AF013970	Homo sapiens MTG8-like protein (MTGR1) mRNA, complete cds	66.55	70
M467 A7	H-AF014807	Homo sapiens phosphatidylinositol synthase (PIS) mRNA, complete cds	23.54	29.0kDa
D2	H-AF015257	Homo sapiens flow-induced endothelial G protein-coupled receptor (FEG-1) mRNA, complete cds	41.36	40
M422 B5	H-AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	40.92	49.0kDa
A6	H-AF017656	Homo sapiens G protein beta 5 subunit mRNA, complete cds	38.94	48
E1	H-AF017995	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds	61.27	52
G1	H-AF019612	Homo sapiens S2P mRNA, complete cds	57.2	57
D3	H-AF020591	Homo sapiens zinc finger protein mRNA, complete cds	78.76	74

A7	H-AF022385	Homo sapiens apoptosis-related protein TFAR15 (TFAR15) mRNA, complete cds	23.43	33
H6	H-AF024714	Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds	37.84	48
B1	H-AF025527	Homo sapiens leucocyte immunoglobulin-like receptor-4 (LIR-4) mRNA, complete cds	48.4	47
M424 B4	H-AF025532	Homo sapiens leucocyte immunoglobulin-like receptor-5 (LIR-5) mRNA, complete cds	49.39	59.0kDa
H5	H-AF026071	Homo sapiens soluble death receptor 3 beta (DR3) mRNA, complete cds	30.58	50
M428 A1	H-AF026273	Homo sapiens interleukin-1 receptor-associated kinase-2 mRNA, complete cds	65.01	68.0kDa
B6	H-AF026293	Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cds	58.96	58
B5	H-AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	45.43	50
B2	H-AF027204	Homo sapiens putative tetraspan transmembrane protein L6H (TM4SF5) mRNA, complete cds	21.78	27
M426 D3	H-AF028008	Homo sapiens SPI-like zinc finger transcription factor SLP mRNA, complete cds	56.43	64.0kDa
B1	H-AF029232	Homo sapiens calpamodulin (CalpM) mRNA, complete cds	70.62	70
M422 A7	H-AF029761	Homo sapiens decoy receptor 2 mRNA, complete cds	42.57	50.0kDa
M477 F3	H-AF029893	Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase mRNA, complete cds	45.76	50.0kDa
C5	H-AF032437	Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds	51.92	50
M416 F3	H-AF035824	Homo sapiens vesicle soluble NSF attachment protein receptor (VT11) mRNA, complete cds	25.63	36.0kDa
F3	H-AF037335	Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds	39.05	39
G1	H-AF039019	Homo sapiens zinc finger DNA binding protein 89 kDa (ZBP-89) mRNA, complete cds	87.45	87
G1	H-AF039136	Homo sapiens Fas binding protein (hDaxx) mRNA, complete cds	81.51	98

A7	H-AF040705	Homo sapiens putative tumor suppressor protein unspliced form (Fus-2) mRNA, complete cds	31.57	41
M469 F1	H-AF040958	Homo sapiens lysosomal neuraminidase precursor, mRNA, complete cds	45.76	46.0kDa
G2	H-AF043472	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (Kv9.3) mRNA, complete cds	54.12	64
E2	H-AJ001340	Homo sapiens mRNA for U3 snoRNP associated 55 kDa protein	52.36	60
G1	H-D00096	Transtyretin (prealbumin)	16.28	20
C4	H-D00408	Cytochrome P450 IIIA7 (P450-HFLa)	55.44	64
M302 E7	H-D00682	cofilin	18.37	30
M383 G2	H-D00726	ferrochelatase	46.64	50.0kDa
M383 C3	H-D00760	proteasome, subunit HC3	25.85	34.0kDa
M305 B4	H-D00761	proteasome, subunit HC5	26.62	33
M266 F7	H-D00763	proteasome, subunit HC9	28.82	33
E2	H-D00860	Phosphoribosyl pyrophosphate synthetase subunit I	35.09	47
215-13	H-D10522	human mRNA for 80K-L protein	35	36.59
M423 F5	H-D11086	Interleukin 2 receptor gamma chain	40.7	45.0kDa
M248 D2	H-D11094	positive modulator of HIV tat-mediated transactivation	47.74	40.0kDa
G3	H-D11428	Peripheral myelin protein 22	17.71	17
M424 D3	H-D13168	Human gene for endothelin-B receptor (hET-BR)	48.73	48.0kDa
M271 B8	H-D13315	glyoxalase I, LACTOYLGLUTATHIONE LYASE. CATALYZES THE CONVERSION OF HEMIMERCAPTAL, FORMED FROM METHYLGLYOXAL AND GLUTATHIONE, TO S-LACTOYLGLUTATHIONE.	20.35	34.0kDa
M306 F1	H-D13627	hypothetical protein (GB:D13627)	60.39	90
M248 D1	H-D13630	hypothetical protein (GB:D13630), Human mRNA for KIAA0005 gene, complete cds	46.2	49
M270 D5	H-D13634	hypothetical protein (GB:D13634)	34.65	42.0kDa
M250 D2	H-D13642	hypothetical protein (GB:D13642), Human mRNA for KIAA0017 gene, complete cds	44	48.0kDa
M250 E6	H-D13748	translation initiation factor 4A	44.77	49.0kDa
M305 C3	H-D13892	carboxyl methyltransferase, aspartate	25.19	34
D1	H-D13900	enoyl-Coenzyme A hydratase, short chain, mitochondrial	32.01	58

E1	H-D14446	Human HFREP-1 mRNA for unknown protein, complete cds	34.43	40
I67-14	H-D14497	H.sapiens (Ewing's sarcoma cell line) mRNA encoding open reading frame	51.44	64
M266 D2	H-D14520	basic transcription element-binding protein 2	24.2	33.0kDa
M318 D2	H-D14658	hypothetical protein (GB:D14658)	13.64	17
D2	H-D14661	Human mRNA for KIAA0105 gene, complete cds	16.72	28
M236 E2	H-D14662	HYPOTHETICAL 29.5 KD PROTEIN IN UBP13-KIP1 INTERGENIC REGION [Saccharomyces cerevisiae]	24.75	36.0kDa
M271 G6	H-D14695	hypothetical protein (GB:D14695), Human mRNA for KIAA0025 gene, complete cds.	43.12	50.0kDa
M311 A3	H-D14696	hypothetical protein (GB:D14696)	25.74	30.0kDa
H3	H-D14697	Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	46.2	55
M271 E7	H-D14705	catenin, alpha 2(E). Catenin (cadherin-associated protein), alpha 1 (102kD). ASSOCIATES WITH THE CYTOPLASMIC DOMAIN OF A VARIETY OF CADHERINS.	99.77	110
M236 A6	H-D14811	hypothetical protein (GB:D14811)	30.25	42
M250 A3	H-D14812	hypothetical protein (GB:D14812), Human mRNA for KIAA0026 gene, complete cds		
A5	H-D14874	Human mRNA for adrenomedullin, complete cds	20.46	33
F3	H-D14887	Human mRNA for TFIIA-42, complete cds	41.47	50
M250 H6	H-D16234	phospholipase C, alpha , PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR [Homo sapiens]	55.66	56.0kDa
M305 B1	H-D16480	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase trifunctional protein, alpha-subunit, mitochondrial	84.04	84

M271 G2	H-D16481	3-ketoacyl-CoA thiolase, beta subunit, mitochondrial, Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit		
H1	H-D16626	Histidine ammonia-lyase	72.38	64
A2	H-D17532	Human mRNA for RCK, complete cds	52.03	53
M266 F4	H-D17554	DNA-binding protein TAX	31.79	38
M248 A3	H-D21235	xeroderma pigmentosum group C repair complementing protein HHR23A	40.04	55
M235 E1	H-D21261	SM22-ALPHA HOMOLOG, hypothetical protein (GB:D21261)	22	31
M311 E1	H-D21262	hypothetical protein (GB:D21262)	77.950	63
M466 B4	H-D21853	Human mRNA for KIAA0111 gene, complete cds	45.32	49.0kDa
M311 H3	H-D23660	ribosomal protein L4	47.08	47
M419 E1	H-D26309	human mRNA for LIMK (LIM kinase)	71.240	75.0kDa
M271 B9	H-D26362	hypothetical protein (GB:D26362), Human mRNA for KIAA0043 gene, complete cds	79.97	70
M361 H2	H-D26598	proteasome, subunit HsC10-II	22.66	33.0kDa
M302 G4	H-D26599	proteasome, subunit HsC7-I	22.22	34
G1	H-D26600	Human mRNA for proteasome subunit HsN3, complete cds	29.15	36
G9	H-D28540	hypothetical protein, CDC10 homolog	44.77	60
M266 A5	H-D29011	proteasome, subunit X	22.99	23
M236 F3	H-D29012	Proteasome (prosome, macropain) delta subunit, beta type, 6	26.4	32.0kDa
C1	H-D30037	Human mRNA for phosphatidylinositol transfer protein (PI-TPbeta), complete cds	29.92	38
M250 H4	H-D30655	translation initiation factor 4AII, and ribosomal binding protein	44.88	45.0kDa
167-26	H-D30742	human mRNA for calmodulin-dependent protein kinase IV	52.10	55
M236 A4	H-D31767	hypothetical protein (GB:D31767), Human mRNA for KIAA0058 gene, complete cds	18.59	30
E1	H-D31883	Human mRNA for KIAA0059 gene, complete cds	50.93	64
G2	H-D32129	MHC class I protein HLA-A	40.26	50
M422 A6	H-D37965	Human mRNA for PDGF receptor beta-like tumor suppressor (PRLTS), complete cds	41.36	45.0kDa

M305 H4	H-D38047	26S proteasome regulatory subunit P31	28.340	34.0kDa
M423 B2	H-D38081	Thromboxane A2 receptor	37.84	45.0kDa
M317 D3	H-D38305	ErbB-2 transducer	38.06	49
M270 A8	H-D38583	calgizzarin, Human mRNA for calgizzarin, complete cds	11.66	12
M270 A6	H-D42038	hypothetical protein (GB:D42038), Human mRNA for KIAA0087 gene, complete cds	15.29	27
M318 F3	H-D42085	hypothetical protein (GB:D42085)	90.2	100
M311 C2	H-D43642	YL-1 protein homolog	40.15	36
E1	H-D45213	Human mRNA for zinc finger protein, complete cds	12.87	20
M236 B2	H-D45248	proteasome activator hPA28, subunit beta , may be cell adhesion protein	26.4	38
H3	H-D45887	Human mRNA for calmodulin, complete cds	16.5	20
166-3	H-D45906	human mRNA for LIMK-2	70	70.25
A7	H-D49357	Human mRNA for S-adenosylmethionine synthetase, complete cds	43.56	51
C5	H-D49489	Human mRNA for protein disulfide isomerase-related protein P5, complete cds	48.51	54
M482 E2	H-D49958	Human fetus brain mRNA for membrane glycoprotein M6, complete cds	30.69	32.0kDa
M305 G5	H-D50063	proteasome, subunit p40	35.75	39
M250 B6	H-D50310	cyclin I, Human mRNA for cyclin I, complete cds	41.58	47
E3	H-D50419	Homo sapiens mRNA for OTK18, complete cds	78.32	64
M298 B1	H-D50495	transcription elongation factor h-SII-T1 (GB:D50495)	33	33.0kDa
M302 A3	H-D50840	ceramide glucosyltransferase	43.45	44
167-40	H-D50863	human mRNA for TESK1	68.9 3	70
166-28	H-D50927	human myeloblast mRNA for KIAA0137 gene	60.46	64
D1	H-D63521	Homo sapiens mRNA for LECT2 precursor, complete cds	16.72	16
M302 A5	H-D78134	glycine-rich binding protein CIRP	19.03	30.0kDa
M313 E5	H-D78275	proteasome subunit p42	42.9	48.0kDa
B3	H-D79205	Human mRNA for ribosomal protein L39, complete cds	5.72	10
A4	H-D79206	Human gene for ryudocan core protein, exon1-5, complete cds	21.89	33
A1	H-D80008	Human mRNA for KIAA0186 gene, complete cds	21.67	32
M298 H4	H-D83004	ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product	16.83	32.0kDa

C3	H-D83702	Human brain mRNA for photolyase homolog, complete cds	64.57	64
M306 A1	H-D83735	neutral calponin	34.1	34.0kDa
H2	H-D86322	Homo sapiens mRNA for calmegin, complete cds	67.21	64
B1	H-D86979	Human mRNA for KIAA0226 gene, complete cds	82.72	82
169-16	H-D87116	dual specificity mitogen-activated protein kinase kinase 3	38.24	42
166-27	H-D87119	human cancellous bone osteoblast mRNA for GS3955	37.80	40
E2	H-D88308	Homo sapiens mRNA for very-long-chain acyl-CoA synthetase, complete cds	68.31	64
166-26	H-D89077	human mRNA for Src-like adapter protein	30.43	38
M440 H2	H-D89479	Homo sapiens mRNA for ST1B2, complete cds	32.67	38.0kDa
H1	H-D90086	Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10	39.6	35
M362 F1	H-D90209	DNA-binding protein TAXREB67	38.72	48.0kDa
M316 B2	H-J00068	actin, alpha 1, skeletal muscle	41.58	50
M250 B2	H-J00194	major histocompatibility complex, MHC class II, DR alpha	28.05	36.0kDa
G2	H-J00212	Interferon, alpha 21	20.9	30
G1	H-J00287	Human pepsinogen gene	42.79	48
M298 C2	H-J02611	apolipoprotein D	20.9	31.0kDa
M266 C4	H-J02683	ADP/ATP carrier protein	32.89	36
M383 H2	H-J02685	plasminogen activator inhibitor, placenta	45.76	50.0kDa
167-3	H-J02853	"casein kinase II, alpha chain"	43.08	50
E3	H-J02854	Human 20-kDa myosin light chain (MLC-2) mRNA, complete cds	19.03	31
M248 F3	H-J02874	fatty-acid-binding protein 4, adipocyte, LIPID TRANSPORT PROTEIN IN ADIPOCYTES	14.63	17
M235 D5	H-J02939	antigen 4F2, heavy chain	58.3	58
C3	H-J02943	Corticosteroid binding globulin	44.66	50
M248 F2	H-J02966	adenine nucleotide translocator 1 (skeletal muscle) [ANT1], CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.	32.78	33
E1	H-J02982	Glycophorin B	10.12	20
167-91	H-J03075	"protein kinase c substrate, 80 kD protein heavy chain"	58.04	98
M266 A3	H-J03191	profilin 1	15.51	17.0kDa
M248 H4	H-J03231	glucose-6-phosphate dehydrogenase [G6PD]	56.76	51

M266 F2	H-J03459	LEUKOTRIENE A-4 HYDROLASE [Homo sapiens]	67.32	64
A2	H-J03460	Prolactin-induced protein	16.17	26
M271 E5	H-J03799	laminin receptor 1, Laminin receptor (2H5 epitope). 40S RIBOSOMAL PROTEIN SA [Homo sapiens].	32.56	
M440 A4	H-J03890	Human pulmonary surfactant protein C (SP-C) and pulmonary surfactant protein C1 (SP-C1) genes, complete cds	21.78	30.0kDa
M271 D8	H-J03934	NAD(P)H menadione oxidoreductase 1, dioxin- inducible. INVOLVED IN DETOXICATION PATHWAYS.	30.25	38
M271 A8	H-J04031	trifunctional enzyme (GB:J04031). C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC [Homo sapiens]	102.96	117.0kDa
M305 F6	H-J04046	calmodulin 3 [CALM3]	16.5	20
M305 G7	H-J04071	cytotoxic T-lymphocyte- associated serine esterase 1 (cathepsin G-like 1, granzyme B) [CTLA1]	27.28	38
M311 D2	H-J04183	lysosomal-associated membrane protein 2	44.99	47
M300 F4	H-J04205	Sjogren syndrome antigen B	44.99	51.0kDa
M416 G8	H-J04430	Acid phosphatase 5, tartrate resistant	35.64	45.0kDa
B1	H-J04501	Glycogen synthase 1 (muscle)	81.18	81
M313 B5	H-J04543	synexin	51.37	51
B1	H-J04605	Peptidase D	54.34	55
M250 C6	H-J04615	small nuclear ribonucleoprotein SM-D, ROLE IN THE PRE- mRNA SPLICING OR IN SNRNPSTRUCTURE.	26.51	34.0kDa
M248 E2	H-J04964	steroid sulfatase (microsomal) [STS]	64.24	60.0kDa
M250 A7	H-J05249	replication protein A, 32 kDa subunit , REQUIRED FOR SV 40 DNA REPLICATION IN VITRO, RP-A IS SINGLE- STRANDED DNA-BINDING PROTEIN.	29.81	36.0kDa
F1	H-J05272	IMP (inosine monophosphate) dehydrogenase 1	56.65	51
169-15	H-J05401	"creatine kinase, sarcomeric mitochondrial precursor"	50	46.16
M266 E4	H-J05448	RNA polymerase II, subunit B33	30.36	35.0kDa
M305 C2	H-K00558	tubulin, alpha k1 [TUBA*]	49.72	52.0kDa
M416 H7	H-K01571	Human T-cell receptor active beta-chain, mRNA from cell line MOLT-3, complete cds	34.43	36.0kDa

M311 E4	H-K01763	haptoglobin	38.28	47.0kDa
G5	H-K02100	Human ornithine transcarbamylase (OTC) mRNA, complete coding sequence	39.05	47
M302 D5	H-K02574	purine nucleoside phosphorylase	31.9	36.0kDa
169-39	H-K02581	"thymidine kinase, cytosolic"	34	25.81
M248 E4	H-K03020	phenylalanine hydroxylase [PAH]	49.83	50
M556 B3	H-K03191	Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide I	56.43	53.0kDa
H2	H-L00190	Antithrombin III	51.15	55
169-62	H-L01087	"protein kinase c, theta type"	80	77.7
M318 C2	H-L01124	ribosomal protein S13	16.72	28
M313 F1	H-L02321	glutathione S-transferase M5	24.09	28
M305 E5	H-L02426	protease 26S, regulatory subunit 4	48.51	53
M302 D4	H-L02547	cleavage stimulation factor, 50 kDa subunit	47.52	50.0kDa
M266 H7	H-L02648	transcobalamin II	47.08	48.0kDa
E2	H-L02932	Human peroxisome proliferator activated receptor mRNA, complete cds	51.59	59
M270 A1	H-L03380	gonadotropin-releasing hormone receptor [GRHR], THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS	36.19	36
M270 H1	H-L03411	RD protein [RDBP], Radin blood group	41.91	59.0kDa
D3	H-L03426	Human XE7 mRNA, complete alternate coding regions	42.46	45
B1	H-L03785	Myosin, light polypeptide 5, regulatory	19.14	32
A7	H-L04483	ribosomal protein S21	9.24	34
M416 B2	H-L05147	Human dual specificity phosphatase tyrosine/serine mRNA, complete cds	20.46	30.0kDa
215-38	H-L05624	dual specificity mitogen-activated protein kinase kinase 1	50	43.30
M271 D4	H-L06132	anion channel, voltage-gated, isoform 1. FORMS A CHANNEL THROUGH THE CELL MEMBRANE, THAT ALLOWS DIFFUSION FROM SMALL HYDROPHYLIC MOLECULES.	31.24	37
169-27	H-L06139	tyrosine-protein kinase receptor TIE-2 precursor	125	123.7
H1	H-L06147	Human (clone SY11) golgin-95 mRNA, complete cds	68.31	68
M250 A1	H-L06419	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) [PLOD]	80.08	80.0kDa
M236 F6	H-L06498	ribosomal protein S20	13.2	23.0kDa
M318 D1	H-L06499	ribosomal protein L37a	10.23	27

M270 D1	H-L07414	CD40 antigen ligand [CD40LG], INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.	28.82	36
M298 A6	H-L07548	aminoacylase 1	44.99	52.0kDa
M424 C3	H-L07592	Human peroxisome proliferator activated receptor mRNA, complete cds	48.62	48.0kDa
M298 G6	H-L07633	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [PSME1]	27.5	33.0kDa
M318 B1	H-L08096	CD70 antigen (CD27 ligand) [CD70]	21.34	28
D2	H-L08187	cytokine receptor EBI3	25.3	42
M313 F4	H-L08850	amyloid, non-A beta component, Alzheimer's disease	15.51	31.0kDa
M426 E1	H-L08895	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	52.14	60.0kDa
M266 A8	H-L09235	ATPase, vacuolar	67.98	64.0kDa
M266 D1	H-L09604	differentiation-dependent intestinal membrane A4 protein (Homo sapiens)	16.83	17.0kDa
M317 C1	H-L10338	sodium channel, voltage-gated, type I, beta polypeptide [SCN1B]	24.09	24
M317 E1	H-L10717	tyrosine-protein kinase ITK/TSK	68.270	68.0kDa
M300 B5	H-L10820	formyl peptide receptor 1 [FPR1]	38.61	37
M312 A4	H-L10838	pre-mRNA splicing factor SRp20	18.15	31.0kDa
M300 A5	H-L10918	chemokine (C-C) receptor 1 [CMKBR1]	39.16	30
M311 F2	H-L11245	complement component 4-binding protein, beta	27.83	30
M266 B7	H-L11353	neurofibromatosis 2 (bilateral acoustic neuroma) [NF2]	65.56	63.0kDa
M311 B3	H-L11667	cyclophilin 40	40.81	50.0kDa
215-49	H-L11695	serine/threonine-protein kinase receptor R4 precursor	64	55.40
M466 C2	H-L11931	Human cytosolic serine hydroxymethyltransferase (SHMT) mRNA, complete cds	53.24	56.0kDa
M271 B7	H-L12168	ADENYLYL CYCLASE- ASSOCIATED PROTEIN 1 [Homo sapiens]	52.36	60.0kDa
M416 D4	H-L12964	Interleukin-activated receptor, homolog of mouse Ly63	28.16	38.0kDa
B3	H-L13203	Human HNF-3/fork-head homolog-3 HFH-3 mRNA, complete cds	38.72	49
D2	H-L13744	Human AF-9 mRNA, complete cds	62.59	63
167-8	H-L13943	glycerol kinase	60	57.71
M311 G3	H-L13974	leucine zipper protein (GB:L13974)	41.14	51

M271 H5	H-L13977	LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR [Homo sapiens].	54.67	57
M270 G2	H-L14283	protein kinase C, zeta [PRKCZ], SERINE- AND THREONINE-SPECIFIC ENZYME.	65.23	98
M235 A3	H-L14286	antioxidant protein, thiol-specific	21.89	32.0kDa
M426 H3	H-L14778	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha){alternative products}	57.42	60.0kDa
B4	H-L15702	complement factor B	84.15	100
M426 A4	H-L16794	Human transcription factor (MEF2) mRNA, complete cds	57.42	60.0kDa
215-25	H-L16862	g protein-coupled receptor kinase GRK6	70	63.4
167-74	H-L16991	thymidylate kinase	36	23.39
169-3	H-L18964	"protein kinase c, iota type"	80	64.64
M305 E2	H-L18972	hypothetical protein (GB:L18972)	75.24	78
M426 D4	H-L19067	Human NF-kappa-B transcription factor p65 subunit mRNA, complete cds	59.18	63.0kDa
215-26	H-L19268	Homo sapiens myotonic dystrophy associated protein kinase mRNA	70	68.71
M271 E1	H-L19297	carbonic anhydrase V [CA5], Mitochondrial carbonic anhydrase. REVERSIBLE HYDRATATION OF CARBON DIOXIDE.	33.66	42
M298 G4	H-L19437	transaldolase	37.18	39.0kDa
M423 C4	H-L19593	Interleukin 8 receptor, beta	39.71	41.0kDa
G1	H-L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds	12.76	13
G2	H-L19739	metallopanstimulin I	9.35	32
M302 E3	H-L19871	activating transcription factor 3	20.02	36.0kDa
167-86	H-L20422	14-3-3 protein eta	34	27.1 3
M440 B2	H-L20492	Human gamma-glutamyl transpeptidase mRNA, complete cds	24.86	35.0kDa
M315 B1	H-L20688	GDP-dissociation inhibitor protein rhoA	22.22	32
M271 H3	H-L20941	ferritin, heavy polypeptide. FERRITIN IS AN INTRACELLULAR MOLECULE THAT STORES IRON IN A SOLUBLE, NONTOXIC, READILY AVAILABLE FORM.	20.24	32
M235 B7	H-L21893	Na+/taurocholate cotransporter, STRICTLY DEPENDENT ON THE		

F1	H-L21934	Sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase)	60.61	60
C2	H-L22075	Human guanine nucleotide regulatory protein (G13) mRNA, complete cds	41.58	50
169-18	H-L22206	vasopressin v2 receptor	60	58.00
M421 A10	H-L22214	Human adenosine A1 receptor (ADORA1) mRNA exons 1-6, complete cds	35.97	38.0kDa
M424 F1	H-L23959	Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds	45.21	53.0kDa
C2	H-L24498	Human gadd45 gene, complete cds	18.26	28
M302 E2	H-L25080	proto-oncogene rhoA, multidrug resistance protein	21.34	31
M270 B8	H-L25081	guanine nucleotide-binding and transforming protein rhoC, Aplysia ras-related homolog 9	21.34	30
M236 E3	H-L25085	Sec61 complex, beta subunit, PROTEIN TRANSLOCATION IN THE ENDOPLASMIC RETICULUM	10.67	19
167-85	H-L25610	cyclin-dependent kinase inhibitor 1	32	18.11
B2	H-L25610	cyclin-dependent kinase inhibitor 1	18.110	40
M297 H2	H-L26232	cathepsin A/phospholipid transfer protein	54.34	64.0kDa
167-4	H-L26318	stress-activated protein kinase JNK1	52	42.31
M428 F1	H-L27586	Human TR4 orphan receptor mRNA, complete cds	67.76	67.0kDa
M302 E5	H-L27711	protein phosphatase KAP1	23.43	28
M250 A6	H-L28010	Homo sapiens HnRNP F protein mRNA, complete cds,		
F1	H-L28821	Alpha mannosidase II isozyme	87.67	87
167-89	H-L28824	tyrosine-protein kinase SYK	70	69.92
M298 E6	H-L28997	ADP-ribosylation factor-like gene 1	20.02	33.0kDa
D4	H-L29219	Homo sapiens clk1 mRNA, complete cds	53.35	60
169-63	H-L29222	Homo sapiens clk1 mRNA	25	15.0 3
M429 B3	H-L29277	Signal transducer and activator of transcription 3 (acute-phase response factor)	84.81	88.0kDa
C1	H-L29433	Human factor X (blood coagulation factor) gene	53.79	64
G3	H-L31860	Glycophorin A	16.61	26
D1	H-L31881	Nuclear factor I/X (CCAAT-binding transcription factor)	48.62	48
169-13	H-L31951	human protein kinase (JNK2) mRNA	55	46.71

A1	H-L32179	Arylacetamide deacetylase (esterase)	44	50
B2	H-L33404	Human stratum corneum chymotryptic enzyme mRNA, complete cds	27.94	36
M312 D3	H-L33799	procollagen C-proteinase enhancer	49.5	51.0kDa
169-77	H-L33801	human protein kinase mRNA GSK-3	55	46.27
M305 D6	H-L34041	L-glycerol-3-phosphate:NAD+ oxidoreductase	38.5	42.0kDa
B4	H-L34355	Homo sapiens (clone p4) 50 kD dystrophin-associated glycoprotein mRNA, complete cds	42.68	47
M297 B3	H-L35013	spliceosomal protein SAP 49	46.75	52.0kDa
167-32	H-L35253	human CSaids binding protein (CSBP1) mRNA	52	39.67
M266 D6	H-L35545	C/activated protein C receptor, endothelial	26.29	38.0kDa
M300 F1	H-L35594	autotaxin	100.76	91.0kDa
M318 E2	H-L36720	bystin	33.77	29
M305 H2	H-L37127	RNA polymerase II	12.98	16
M300 D1	H-L38490	ADP-ribosylation factor (GB:L38490)	22.22	32
M318 E1	H-L38941	ribosomal protein L34	12.98	18
C2	H-L38969	Homo sapiens thrombospondin 3 (THBS3) gene, complete cds	105.27	110
M476 F4	H-L39060	Homo sapiens transcription factor SL1 mRNA, complete cds	49.61	53.0kDa
M300 E4	H-L40399	hypothetical protein (GB:L40399)	29.26	36
E3	H-L40802	Homo sapiens 17-beta-hydroxysteroid dehydrogenase (17-HSD) gene	42.68	60
M478 F1	H-L40904	H. sapiens peroxisome proliferator activated receptor gamma, complete cds	52.69	60.0kDa
M306 C2	H-L41268	natural killer associated transcript 2 [NKAT2*]	37.62	40
M306 E2	H-L41270	natural killer associated transcript 4 [NKAT4*]	50.16	65.0kDa
M306 F2	H-L41347	natural killer associated transcript 5 [NKAT5*]	33.55	40
M468 C3	H-L41351	Homo sapiens prostaticin mRNA, complete cds	37.84	45.0kDa
169-53	H-L41816	Homo sapiens cam kinase I mRNA	48	40.77
167-25	H-L41939	tyrosine-protein kinase receptor EPH-3 precursor	108	108.6
C3	H-L42374	Homo sapiens protein phosphatase 2A B56-beta (PP2A) mRNA, complete cds	54.78	64
M306 B1	H-L42531	glutathione synthetase	52.25	54.0kDa

M302 F6	H-L42856	RNA polymerase II transcription factor SIII, p18 subunit	13.09	20.0kDa
M313 C7	H-L76200	guanylate kinase (GUK1)	21.78	32.0kDa
M428 E1	H-L76702	Homo sapiens protein phosphatase 2A B56-delta (PP2A) mRNA, complete cds	66.33	68.0kDa
M478 A1	H-L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds	51.48	60.0kDa
166-52	H-L77213	H.sapiens phosphomevalonate kinase mRNA	34	21.19
169-64	H-L77964	H.sapiens ERK3 mRNA	100	79.38
M360 C3	H-M10050	fatty-acid-binding protein 2, intestinal	14.08	20.0kDa
D5	H-M10050	fatty-acid-binding protein 2, intestinal	14.08	36
M421 E7	H-M10058	Asialoglycoprotein receptor 1	32.12	48.0kDa
M429 D3	H-M10901	Glucocorticoid receptor	85.58	85.0kDa
M312 G1	H-M11025	asialoglycoprotein receptor 2	34.32	34.0kDa
167-44	H-M11026	interferon alpha-4 precursor	33	20.86
F2	H-M11321	Human group-specific component vitamin D-binding protein mRNA, complete cds	52.25	56
M236 B5	H-M11354	histone H3.2, CENTRAL ROLE IN NUCLEOSOME FORMATION.	15.07	24
M236 G2	H-M11433	retinol-binding protein 1, cellular transport protein	14.96	28
M270 G7	H-M11560	aldolase A , FRUCTOSE-BISPHOSPHATE ALDOLASE A [Homo sapiens]	40.15	40
H3	H-M11717	Human heat shock protein (hsp 70) gene, complete cds	70.51	60
E1	H-M12523	Human serum albumin (ALB) gene, complete cds	67.1	70
B5	H-M12963	Alcohol dehydrogenase 1 (class I), alpha polypeptide	41.36	48
D6	H-M13228		51.15	50
D4	H-M13981	Inhibin, alpha	40.37	50
M236 G4	H-M13982	interleukin 4 [IL4] precursor, B-cell activator	16.94	30
M271 B6	H-M14043	lipocortin II, Annexin II (lipocortin II). CALCIUM-REGULATED MEMBRANE-BINDING PROTEIN	37.4	45.0kDa
M271 F4	H-M14218	argininosuccinate lyase	51.04	56
M297 A3	H-M14221	cathepsin B	37.4	32.0kDa
M305 B2	H-M14328	enolase, alpha	47.85	50
167-54	H-M14333	human c-syn protooncogene	60	59.14
167-51	H-M14505	H.sapiens mRNA (open reading frame; patient SK29(AV))	36	33.40
215-74	H-M14676	human src-like kinase (slk) mRNA	60	59.14

167-55	H-M14780	"creatine kinase, m chain"	52	41.98
M416 F8	H-M15059	Fc fragment of IgE, low affinity II, receptor for (CD23A)	35.42	45.0kDa
M271 F1	H-M15182	glucuronidase, beta [GUSB], PLAYS AN IMPORTANT ROLE IN THE DEGRADATION OF DERMATAN AND KERATAN SULFATES.	71.72	72
215-37	H-M15465	human pyruvate kinase type L mRNA	64	59.80
M298 A4	H-M15796	cyclin	28.82	43.0kDa
C3	H-M15800	Mal, T-cell differentiation protein	16.94	17
M440 E1	H-M15841	Human U2 small nuclear RNA-associated B" antigen mRNA, complete cds	24.86	34.0kDa
M248 C3	H-M15887	endozepine	9.68	15.0kDa
M463 A2	H-M15990	human c-yes-1 mRNA	59.800	65.0kDa
M418 E2	H-M16038	tyrosine-protein kinase LYN	56.390	64.0kDa
M266 D3	H-M16342	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 [Homo sapiens]; small nuclear ribonucleoprotein, polypeptide C	32.01	49
167-20	H-M16591	tyrosine-protein kinase HCK	60	55.62
C7	H-M16591	tyrosine-protein kinase HCK	55.620	70
M305 E7	H-M16660	heat shock 90kD protein 1, beta [HSPCB]	79.75	80
167-65	H-M16750	PIM-1 proto-oncogene serine/threonine-protein kinase	38	34.50
M311 A1	H-M16827	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain	46.42	50.0kDa
D3	H-M16961	Alpha-2-HS-glycoprotein alpha and beta chain	40.48	50
D3	H-M16974	Complement component 8, alpha polypeptide	64.35	55
M248 C2	H-M17017	INTERLEUKIN-8 PRECURSOR [Homo sapiens]	11	11
M305 E4	H-M17885	ribosomal phosphoprotein P0, acidic	34.98	37.0kDa
M339 E2	H-M17887	ribosomal phosphoprotein P2	12.76	19.0kDa
M248 D5	H-M18731	galactose-1-phosphate uridylyltransferase [GALT]	41.91	42
F2	H-M19309	Troponin T1, skeletal, slow	30.69	40
M385 E2	H-M19713	tropomyosin, alpha, muscle	31.35	41.0kDa
167-79	H-M19722	proto-oncogene tyrosine-protein kinase FGR	64	58.26
M248 H1	H-M20560	Annexin III (lipocortin III), INHIBITOR OF PHOSPHOLIPASE A2	35.64	37
M235 H1	H-M20681	GLUCOSE TRANSPORTER TYPE 3, BRAIN	54.67	50
167-29	H-M21616	beta platelet-derived growth factor receptor precursor	121	121.7

M305 A3	H-M21812	myosin light chain 2	18.81	30
167-30	H-M22146	"40S ribosomal protein S4, x isoform"	34	26.91
M302 D6	H-M22430	phospholipase A2 RASF-A	15.95	31.0kDa
E2	H-M22491	Bone morphogenetic protein 3 (osteogenic)	52.03	55
M340 A2	H-M22538	NADH-ubiquinone reductase, 24 kDa subunit, mitochondrial	27.5	33
B2	H-M22632	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	47.41	47
B4	H-M22960	Protective protein for beta-galactosidase (galactosialidosis)	52.91	60
M250 C4	H-M22995	ras-related protein RAPIA, member of RAS oncogene family		
B3	H-M23254	Calpain, large polypeptide L2	77.11	77
M266 B4	H-M23613	Nucleophosmin (nucleolar phosphoprotein B23, numatrin), BELIEVED TO BIND SINGLE-STRANDED NUCLEIC ACIDS	32.45	42
M469 D2	H-M23668	Homo sapiens adrenodoxin gene	20.35	25.0kDa
M478 H3	H-M24439	Human liver/bone/kidney-type alkaline phosphatase (ALPL) gene	57.75	64.0kDa
F5	H-M24470	Glucose-6-phosphate dehydrogenase	38.06	44
M270 E5	H-M24898	thyroid hormone triiodothyronine receptor c-erbA, ear-1, Thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog)	67.65	85
D3	H-M24902	Acid phosphatase, prostate	42.57	54
D6	H-M25809	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1	56.32	57
167-77	H-M26252	"pyruvate kinase, M2 isozyme"	60	58.48
M271 F8	H-M26326	keratin 18	47.41	50.0kDa
B1	H-M26901	Human renin gene	44.44	50
M271 G4	H-M27396	asparagine synthetase	61.82	62
M338 B3	H-M27542	globulin, sex hormone-binding	39.200	40
M512 B6	H-M27602	Protease, serine, 2 (trypsin 2)	27.28	36.0kDa
M270 B6	H-M27691	DNA-binding protein CREB, cAMP-responsive	36.08	50
C1	H-M27878	Zinc finger protein 84 (HPF2)	81.29	81
M270 F6	H-M28209	guanine nucleotide-binding protein rab1	22.66	30.0kDa
M512 H5	H-M28210	RAB3A, member RAS oncogene family	24.31	36.0kDa
B3	H-M28214	Homo sapiens GTP-binding protein (RAB3B) mRNA, complete cds	24.2	34

M300 C5	H-M28249	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) [ITGA2]	130.02	130.0kDa
M248 B6	H-M28372	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) [ZNF9]	19.58	28.0kDa
M248 C5	H-M28983	interleukin 1, alpha [IL1A]	29.92	42
M298 C1	H-M29536	translation initiation factor 2, beta subunit	36.74	50.0kDa
M425 A5	H-M29696	Interleukin 7 receptor	50.6	63.0kDa
E1	H-M29960	Human steroid receptor (TR2-11) mRNA, complete cds	66.44	65
M361 D3	H-M29971	6-O-methylguanine-DNA methyltransferase [MGMT]	22.88	33.0kDa
167-67	H-M30448	"casein kinase II, beta chain"	34	23.72
M250 E2	H-M31211	MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE A ISOFORM [Homo sapiens]	22.99	30.0kDa
M311 C4	H-M31452	proline-rich protein	65.78	68
M312 H3	H-M31469	ras-like protein TC4	23.87	32.0kDa
167-41	H-M31606	"phosphorylase B kinase gamma catalytic chain, testis isoform"	50	44.7
B4	H-M31642	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	24.09	36
M416 D8	H-M31932	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	34.98	45.0kDa
M305 A8	H-M32011	neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2) [NCF2]	57.97	58
B2	H-M32315	Human tumor necrosis factor receptor mRNA, complete cds	50.82	60
M266 C2	H-M33374	cell adhesion protein SQM1	14.96	18.0kDa
M431 F1	H-M33375	dihydrodiol dehydrogenase 4	33.99	40.0kDa
G6	H-M33680	Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds	26.07	24
F1	H-M33772	Human fast skeletal muscle troponin C gene	17.71	29
167-15	H-M34065	m-phase inducer phosphatase 3	55	52.10
F4	H-M34079	Human immunodeficiency virus tat transactivator binding protein-1 (tbp-1) mRNA, complete cds	44.55	52
169-86	H-M34181	"cAMP-dependent protein kinase, beta-catalytic subunit"	50	38.68
D1	H-M34379	Elastatase 2, neutrophil	29.48	35
M314 E1	H-M34671	CD59 glycoprotein precursor	14.150	20
M266 C3	H-M35252	CO-029 (GB:M35252)	26.18	30
M315 A4	H-M36035	benzodiazapine receptor (peripheral) [BZRP]	18.7	19
M300 C1	H-M36340	ADP-ribosylation factor 1	20.02	30
M312 C3	H-M36341	ADP-ribosylation factor 2	19.91	29
D6	H-M36634	Vasoactive intestinal peptide	18.81	28

169-26	H-M36881	proto-oncogene tyrosine-protein kinase LCK	60	56.06
167-76	H-M36981	nucleoside diphosphate kinase B	26	16.79
M298 D6	H-M37400	aspartate aminotransferase, cytosolic	45.54	50.0kDa
167-88	H-M37712	galactosyltransferase associated protein kinase P58/GTA	55	48.36
M424 F4	H-M38258	Retinoic acid receptor, gamma 1	50.05	58.0kDa
M266 H3	H-M38690	CD9 antigen, INVOLVED IN PLATELET ACTIVATION AND AGGREGATION.	25.19	26.0kDa
M270 A5	H-M55265	casein kinase II, alpha catalytic subunit	43.12	50
169-74	H-M55284	human protein kinase C-L (PRKCL) mRNA	80	75.09
M512 B3	H-M55514	Potassium voltage-gated channel, shaker-related subfamily, member 4	71.94	100.0kDa
M271 F5	H-M57567	ADP-ribosylation factor 5 [AR5]. INVOLVED IN PROTEIN TRAFFICKING AND ACTS AS AN ALLOSTERIC ACTIVATOR OF CHOLERA TOXIN.	19.91	32.0kDa
M250 D1	H-M57627	interleukin 10 [IL10], SUPPRESSOR FACTOR FOR TH1 IMMUNE RESPONSES (BY SIMILARITY).	19.69	27
M302 D3	H-M57730	EPH-related receptor tyrosine kinase ligand 1 precursor	22.620	36.0kDa
M248 B5	H-M58458	ribosomal protein S4, X-linked [RPS4X]	29.04	36.0kDa
M248 A5	H-M58459	ribosomal protein S4, Y-linked [RPS4Y]	29.04	36
M248 G5	H-M58525	CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM [Homo sapiens], COMT	29.92	36
M482 B2	H-M59916	Sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	69.3	69.0kDa
M390 C1	H-M60091	galactose-1-phosphate uridylyltransferase	41.8	50.0kDa
M316 B1	H-M60314	bone morphogenetic protein 5 [BMP5]	50.05	55
B4	H-M60459	Erythropoietin receptor	55.99	60
C7	H-M60483	Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds	34.1	56
M462 D7	H-M60484	Human protein phosphatase 2A catalytic subunit-beta gene, complete cds	34.1	44.0kDa
A12	H-M60527	deoxycytidine kinase	28.670	50
167-5	H-M60724	human p70 ribosomal S6 kinase alpha-1 mRNA	66	57.82

167-17	H-M60725	human p70 ribosomal S6 kinase alpha-II mRNA	62	55.29
M271 A4	H-M61199	cleavage signal 1, ESTs, Highly similar to CLEAVAGE SIGNAL-1 PROTEIN [Homo sapiens]	27.5	36.0kDa
B1	H-M61733	Homo sapiens erythroid membrane protein 4.1 mRNA, complete cds	70.62	71
M298 A1	H-M61764	tubulin, gamma	49.72	55.0kDa
M422 E2	H-M62505	Complement component 5 receptor 1 (C5a ligand)	38.61	38.0kDa
M313 G5	H-M62810	transcription factor 1, mitochondrial	27.17	35.0kDa
C9	H-M62839	apolipoprotein H	38.06	60
G5	H-M63154	Gastric intrinsic factor (vitamin B synthesis)	45.98	52
167-6	H-M63167	RAC-alpha serine/threonine kinase	64	52.87
B1	H-M63573	Peptidylprolyl isomerase B (cyclophilin B)	23.87	33
M302 H2	H-M63603	phospholamban	5.83	6
M306 D1	H-M63838	interferon, gamma-inducible protein 16	80.3	108
M423 H3	H-M63959	Low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	39.38	48.0kDa
G3	H-M64099	Human gamma-glutamyl transpeptidase-related protein (GGT-Rel) mRNA, complete cds	64.57	52
M475 B8	H-M64673	Human heat shock factor 1 (TCF5) mRNA, complete cds	58.3	65.0kDa
M266 D5	H-M64716	ribosomal protein S25	13.86	17.0kDa
M248 C6	H-M64752	glutamate receptor, ionotropic, AMPA 1 [GRIA1]	99.88	100
M312 G3	H-M64925	palmitoylated membrane protein, erythrocyte, 55 kDa	51.37	51.0kDa
M302 C7	H-M65292	complement factor H-related protein (GB:M65292)	36.41	50
D3	H-M68516	Human protein C inhibitor gene, complete cds	44.77	54
167-27	H-M68520	cell division protein kinase 2	38	32.85
M236 D5	H-M68867	Cellular retinoic acid-binding protein 2, MAY REGULATE THE ACCESS OF RETINOIC ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS.	15.29	19.0kDa
M441 E1	H-M69226	monoamine oxidase A [MAOA]	58.08	64.0kDa
M298 D5	H-M72393	calcium-dependent phospholipid-binding protein [PLA2*]	82.5	117.0kDa
M422 D5	H-M73238	Ciliary neurotrophic factor receptor	41.03	51.0kDa

C1	H-M73255	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS	81.4	81
M422 G6	H-M73481	Human gastrin releasing peptide receptor (GRPR) mRNA, complete cds	42.35	45.0kDa
M235 G6	H-M73499	carboxylesterase, INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.	62.48	90.0kDa
M302 D1	H-M73547	polyposis locus DP1	20.46	28
M300 H4	H-M73969	interleukin 8 receptor, beta [IL8RB]	39.71	36
G1	H-M74491	ADP-ribosylation factor 3	20.02	31
B4	H-M74816		49.5	50
B2	H-M75110	H,K-ATPase, beta subunit	32.12	37
M416 B8	H-M76766	General transcription factor IIB	34.87	44.0kDa
167-18	H-M77198	RAC-beta serine/threonine kinase	64	57.27
167-87	H-M77348	PMEL 17 protein precursor	74	73.55
C4	H-M77698	YY1 transcription factor	45.65	48
M248 G6	H-M80261	apurinic/aprimidinic (abasic) endonuclease [APE], REPAIRS OXIDATIVE DNA DAMAGES IN VITRO	35.09	37.0kDa
169-50	H-M80359	putative serine/threonine-protein kinase P78	80	78.50
M330 H1	H-M80461	immunoglobulin-associated beta (B29) [IGB]	25.370	27.0kDa
169-1	H-M80613	ring3 protein	100	83.01
M298 A2	H-M80783	B12 protein	34.87	43.0kDa
217-1	H-M81457	calpactin I light chain	10	10.74
M422 C6	H-M81589	Homo sapiens serotonin 1D receptor (5-HT1D-) mRNA, complete cds	41.58	41.0kDa
M424 A1	H-M81590	Homo sapiens serotonin 1D receptor (5-HT1D-) mRNA, complete cds	43.01	48.0kDa
M250 H1	H-M81592	gamma-glutamyl carboxylase [GGCX], CONVERTS GLUTAMATE RESIDUES TO GAMMA-CARBOXYGLUTAMATE	83.49	85
M250 F2	H-M81601	TRANSCRIPTION ELONGATION FACTOR S-II [Homo sapiens]	33.22	36.0kDa
C2	H-M81650	Human semenogelin I (SEMG1) gene, complete cds	50.93	52
M266 A4	H-M81757	ribosomal protein S19	16.06	18
169-61	H-M81933	m-phase inducer phosphatase 1	57	57.60
M302 H1	H-M82809	annexin IV	35.42	38.0kDa
M300 C4	H-M83653	cytoplasmic phosphotyrosyl protein phosphatase, type 1	17.49	28.0kDa

169-14	H-M83941	tyrosne-protein kinase receptor ETK1 precursor	108	108.2
F1	H-M84443	Galactokinase 2	50.49	52
M305 H6	H-M84747	interleukin 9 receptor [IL9R]	57.53	58
167-53	H-M86400	14-3-3 protein zeta/delta	33	27.02
M271 C8	H-M86521	transketolase	68.64	68.0kDa
169-51	H-M86699	human kinase (TTK) mRNA	92	92.58
M316 F2	H-M86752	transformation-sensitive protein	59.84	60.0kDa
M270 C8	H-M86921	membrane glycoprotein mb-1, Immunoglobulin-associated alpha, ASSOCIATED TO SURFACE IGM-RECEPTOR; MAY BE INVOLVED IN SIGNAL TRANSDUCTION	24.97	34
A5	H-M87507	Homo sapien interleukin-1 beta convertase (IL1BCE) mRNA, complete cds	44.55	50
M305 B7	H-M88011	glucokinase [GCK]	51.26	60
M305 H1	H-M88279	immunophilin FKBP52	50.6	64.0kDa
M420 F1	H-M88468	mevalonate kinase	43.600	47.0kDa
M305 A7	H-M89913	dUTP pyrophosphatase (dUTPase) [DUT*]	15.62	19
M316 E2	H-M90657	tumor-associated antigen L6	22.33	28
167-31	H-M90813	human D-type cyclin (CCND2) mRNA	36	31.86
A1	H-M91036	H.sapiens G-gamma globin and A-gamma globin genes, complete cds's	16.28	18
G2	H-M91463	Human glucose transporter (GLUT4) gene, complete cds	55.66	52
A1	H-M91670	Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds	24.86	36
E4	H-M92444	Homo sapiens apurinic/aprimidinic endonuclease (HAP1) gene, complete cds	35.09	45
M305 C4	H-M94556	single-stranded DNA-binding protein, mitochondrial	16.39	20
G12	H-M94856	fatty-acid-binding protein homolog	14.96	36
M453 C3	H-M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds	39.82	50.0kDa
M302 F2	H-M95787	smooth muscle protein SM22	22.22	33.0kDa
A1	H-M95809	Human basic transcription factor 62kD subunit (BTF2), complete cds	60.39	64
M271 E8	H-M96982	small nuclear ribonucleoprotein U2 auxiliary factor, 35 kDa , SPLICING FACTOR U2AF 35 KD SUBUNIT. NECESSARY FOR THE SPLICING OF PRE- mRNA.	26.51	39.0kDa

M416 B3	H-M96995	Growth factor receptor-bound protein 2	23.98	32.0kDa
G2	H-M96995	Growth factor receptor-bound protein 2	23.98	49
H4	H-M97016	Bone morphogenetic protein 8 (osteogenic protein 2)	44.33	61
M271 D1	H-M97190	Sp2 transcription factor [SP2], BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY ACTIVATES mRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL RECOGNITION SITES.	54.56	60
M271 C1	H-M97191	Sp3 transcription factor [SP3], BINDS TO GT AND GC BOXES PROMOTERS ELEMENTS. PROBABLE TRANSCRIPTIONAL ACTIVATOR.	71.94	72
M305 C7	H-M97388	transcription repressor (interacting with the TATA-binding protein) [DR1*]	19.47	30
217-13	H-M97675	human transmembrane receptor (ror1) mRNA	100	103.1
B3	H-M97856	Nuclear autoantigenic sperm protein (histone-binding)	86.68	87
M429 G2	H-M97935	Homo sapiens transcription factor ISGF-3 mRNA, complete cds	82.61	89.0kDa
D1	H-M99487	Human prostate-specific membrane antigen (PSM) mRNA, complete cds	82.61	92
M363 A1	H-P0002	riboflavin synthase beta chain (ribE)	17.27	
M363 B1	H-P0004	carbonic anhydrase (icfA)	24.42	
M363 C1	H-P0005	orotidine 5'-phosphate decarboxylase (pyrF)	25.08	
M363 D1	H-P0006	pantoate-beta-alanine ligase (panC)	30.47	
M379 A1	H-P0010-2	chaperone and heat shock protein (groEL)	60.17	
M363 E1	H-P0011	co-chaperone (groES)	13.09	
M363 F1	H-P0012	DNA primase (dnaG)	61.6	
M363 G1	H-P0013	hypothetical protein	38.61	
M363 H1	H-P0014	hypothetical protein	30.36	
M363 A2	H-P0015	hypothetical protein	10.34	
M363 B2	H-P0016	hypothetical protein	9.68	
M363 C2	H-P0017	virB4 homolog (virB4)	86.68	
M363 D2	H-P0018	hypothetical protein	51.7	
M363 E2	H-P0021	hypothetical protein	21.01	
M363 F2	H-P0022	conserved hypothetical integral membrane protein	57.42	
M363 G2	H-P0026	citrate synthase (gltA)	46.97	
M363 H2	H-P0027	isocitrate dehydrogenase (icd)	46.86	

M363 A3	H-P0028	conserved hypothetical secreted protein	19.58	
M363 B3	H-P0030	hypothetical protein	65.34	
M363 C3	H-P0031	hypothetical protein	15.18	
M363 D3	H-P0034	aspartate 1-decarboxylase (panD)	12.98	
M363 E3	H-P0035	conserved hypothetical protein	10.78	
M363 F3	H-P0037	NADH-ubiquinone oxidoreductase subunit	38.72	
M363 G3	H-P0044	GDP-D-mannose dehydratase (rfbD)	42.02	
M363 H3	H-P0047	hydrogenase expression/formation protein (hypE)	36.63	
M363 A4	H-P0048	transcriptional regulator (hypF)	84.7	
M363 B4	H-P0052	hypothetical protein	36.41	
M363 C4	H-P0055	proline permease (putP)	54.67	
M363 D4	H-P0056	delta-1-pyrroline-5-carboxylate dehydrogenase	130.46	
M363 E4	H-P0057	hypothetical protein	7.7	
M363 F4	H-P0063	hypothetical protein	54.67	
M363 G4	H-P0064	hypothetical protein	15.4	
M363 H4	H-P0066	conserved hypothetical ATP-binding protein	91.52	
M363 A5	H-P0067	urease accessory protein (ureH)	29.26	
M363 B5	H-P0068	urease accessory protein (ureG)	22	
M363 C5	H-P0075	urease protein (ureC)	49.06	
M363 D5	H-P0077	peptide chain release factor RF-1 (prfA)	38.83	
M363 E5	H-P0082	methyl-accepting chemotaxis transducer (tlpC)	74.14	
M363 F5	H-P0086	conserved hypothetical protein	49.61	
M363 G5	H-P0087	hypothetical protein	50.38	
M363 H5	H-P0088	RNA polymerase sigma-70 factor (rpoD)	73.92	
M363 A6	H-P0089	pfs protein (pfs)	25.52	
M363 B6	H-P0090	malonyl coenzyme A-acyl carrier protein transacylase (fabD)	34.1	
M363 C6	H-P0093	hypothetical protein	12.21	
M363 D6	H-P0096	phosphoglycerate dehydrogenase	34.65	
M304 A1	H-P0099	methyl-accepting chemotaxis protein (tlpA)	74.36	
M304 B1	H-P0100	conserved hypothetical protein	40.59	
M304 C1	H-P0101	hypothetical protein	27.94	
M304 D1	H-P0104	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	64.02	
M304 E1	H-P0105	conserved hypothetical protein	17.16	
M304 F1	H-P0106	cystathionine gamma-synthase (metB)	41.91	
M304 G1	H-P0107	cysteine synthetase (cysK)	33.77	
M304 H1	H-P0108	hypothetical protein	20.57	
M304 A2	H-P0109	chaperone and heat shock protein 70 (dnaK)	68.31	
M304 B2	H-P0110	co-chaperone and heat shock protein (grpE)	20.9	

M304 C2	H-P0111	hypothetical protein	30.47	
M304 D2	H-P0113	hypothetical protein	10.89	
M304 E2	H-P0114	hypothetical protein	69.19	
M304 F2	H-P0115	flagellin B (flaB)	56.65	
M304 G2	H-P0116	DNA topoisomerase I (topA)	81.07	
M304 H2	H-P0117	conserved hypothetical protein	33.99	
M304 A3	H-P0118	hypothetical protein	43.56	
M304 B3	H-P0119	hypothetical protein	50.82	
M304 C3	H-P0120	hypothetical protein	43.89	
M304 D3	H-P0121	phosphoenolpyruvate synthase (ppsA)	89.43	
M304 E3	H-P0122	hypothetical protein	4.84	
M304 F3	H-P0123	threonyl-tRNA synthetase (thrS)	67.43	
M304 G3	H-P0124	translation initiation factor IF-3 (infC)	22.44	
M304 H3	H-P0125	ribosomal protein L35 (rpl35)	7.15	
M304 A4	H-P0126	ribosomal protein L20 (rpl20)	12.87	
M304 B4	H-P0127	outer membrane protein (omp4)	31.57	
M304 C4	H-P0128	hypothetical protein	4.62	
M304 D4	H-P0129	hypothetical protein	15.62	
M304 E4	H-P0130	hypothetical protein	31.57	
M304 F4	H-P0131	hypothetical protein	3.74	
M304 G4	H-P0132	L-serine deaminase (sdaA)	50.16	
M304 H4	H-P0133	serine transporter (sdaC)	45.54	
M304 A5	H-P0134	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (dhs1)	49.5	
M304 B5	H-P0135	hypothetical protein	4.95	
M304 C5	H-P0136	bacterioferritin comigratory protein (bcp)	16.83	
M304 D5	H-P0137	hypothetical protein	23.32	
M304 E5	H-P0138	conserved hypothetical iron-sulfur protein	53.02	
M304 F5	H-P0139	conserved hypothetical secreted protein	26.73	
M304 G5	H-P0140	L-lactate permease (lctP)	60.5	
M304 H5	H-P0141	L-lactate permease (lctP)	60.72	
M304 A6	H-P0142	A/G-specific adenine glycosylase (mutY)	36.19	
M304 B6	H-P0144	cytochrome c oxidase, heme b and copper-binding subunit, membrane-bound (fixN)	53.79	
M304 C6	H-P0145	cytochrome c oxidase, monoheme subunit, membrane-bound (fixO)	25.63	
M304 D6	H-P0146	cbb3-type cytochrome c oxidase subunit Q (CcoQ)	8.14	
M304 E6	H-P0147	cytochrome c oxidase, diheme subunit, membrane-bound (fixP)	31.57	
M304 F6	H-P0148	hypothetical protein	7.59	
M304 G6	H-P0150	hypothetical protein	21.67	
M304 H6	H-P0152	hypothetical protein	31.68	
M304 A7	H-P0153	recombinase (recA)	38.28	
M304 B7	H-P0154	enolase (eno)	46.97	
M304 C7	H-P0155	hypothetical protein	10.12	

M304 D7	H-P0157	shikimic acid kinase I (aroK)	17.93	
M304 E7	H-P0158	hypothetical protein	35.09	
M304 F7	H-P0159	lipopolysaccharide 1,2-glucosyltransferase (rfaJ)	41.03	
M304 G7	H-P0161	hypothetical protein	4.07	
M304 H7	H-P0162	conserved hypothetical protein	26.51	
M304 A8	H-P0163	delta-aminolevulinic acid dehydratase (hemB)	35.64	
M304 B8	H-P0164	signal-transducing protein, histidine kinase	28.05	
M304 C8	H-P0165	hypothetical protein	19.14	
M304 D8	H-P0166	response regulator (ompR)	24.86	
M304 E8	H-P0167	hypothetical protein	17.38	
M304 F8	H-P0168	hypothetical protein	9.68	
M304 G8	H-P0170	hypothetical protein	27.94	
M304 H8	H-P0171	peptide chain release factor RF-2 (prfB)	40.04	
M304 A9	H-P0172	molybdopterin biosynthesis protein (moeA)	43.12	
M304 B9	H-P0173	flagellar biosynthetic protein (fliR)	28.16	
M304 C9	H-P0174	hypothetical protein	28.49	
M304 D9	H-P0175	cell binding factor 2	33	
M304 E9	H-P0176	fructose-bisphosphate aldolase (tsr)	33.88	
M304 F9	H-P0177	translation elongation factor EF-P (efp)	20.68	
M304 G9	H-P0178	spore coat polysaccharide biosynthesis protein E	37.51	
M304 H9	H-P0179	ABC transporter, ATP-binding protein	23.54	
M304 A10	H-P0180	apolipoprotein N-acyltransferase (cute)	46.86	
M304 B10	H-P0182	lysyl-tRNA synthetase (lysS)	55.22	
M304 C10	H-P0183	serine hydroxymethyltransferase (glyA)	45.87	
M304 D10	H-P0184	hypothetical protein	19.91	
M304 E10	H-P0185	hypothetical protein	29.48	
M304 F10	H-P0186	hypothetical protein	44.55	
M304 G10	H-P0187	hypothetical protein	10.56	
M304 H10	H-P0188	hypothetical protein	3.74	
M304 A11	H-P0189	conserved hypothetical integral membrane protein	19.58	
M304 B11	H-P0190	conserved hypothetical secreted protein	55.33	
M304 C11	H-P0191	fumarate reductase, iron-sulfur subunit (frdB)	27.06	
M304 D11	H-P0192	fumarate reductase, flavoprotein subunit (frdA)	78.65	
M304 E11	H-P0193	fumarate reductase, cytochrome b subunit (frdC)	28.16	
M304 F11	H-P0194	triosephosphate isomerase (tpi)	25.85	

M304 G11	H-P0195	enoyl-(acyl-carrier-protein) reductase (NADH) (fabI)	30.36	
M365 A1	H-P0197	S-adenosylmethionine synthetase 2 (metX)	42.46	
M365 B1	H-P0203	hypothetical protein	10.12	
M365 C1	H-P0209	hypothetical protein	49.61	
M365 D1	H-P0213	glucose inhibited division protein (gidA)	68.42	
M381 E1	H-P0218	hypothetical protein	20.24	
M365 E1	H-P0221	nifU-like protein	35.97	
M365 F1	H-P0227	outer membrane protein (omp5)	76.12	
M365 G1	H-P0228	conserved hypothetical integral membrane protein	43.01	
M365 H1	H-P0230	CTP: CMP-3-deoxy-D-manno-octulosonate-cytidylyl-transferase (kdsB)	26.84	
M365 A2	H-P0233	conserved hypothetical protein	43.01	
M365 B2	H-P0235	conserved hypothetical secreted protein	39.16	
M365 C2	H-P0236	hypothetical protein	13.64	
M365 D2	H-P0238	prolyl-tRNA synthetase (proS)	63.58	
M381 E2	H-P0243	neutrophil activating protein (napA) (bacterioferritin)	15.95	
M365 E2	H-P0244	signal-transducing protein, histidine kinase (atoS)	42.02	
M365 F2	H-P0246	flagellar basal-body P-ring protein (flgI)	37.73	
M365 G2	H-P0247	ATP-dependent RNA helicase, DEAD-box family (deaD)	54.23	
M365 H2	H-P0248	conserved hypothetical protein	39.93	
M379 B1	H-P0249-2	hypothetical protein	19.8	
M379 C1	H-P0250-2	oligopeptide ABC transporter, ATP-binding protein (oppD)	56.87	
M381 A3	H-P0251	oligopeptide ABC transporter, permease protein (oppC)	37.29	
M379 E1	H-P0252-2	outer membrane protein (omp7)	53.68	
M365 A3	H-P0254	outer membrane protein (omp8)	47.52	
M365 B3	H-P0255	adenylosuccinate synthetase (purA)	45.32	
M365 C3	H-P0257	conserved hypothetical secreted protein	24.2	
M365 D3	H-P0259	exonuclease VII, large subunit (xseA)	46.31	
M381 D3	H-P0260	adenine specific DNA methyltransferase (mod)	42.35	
M365 E3	H-P0263	adenine specific DNA methyltransferase (hpaim)	27.83	
M365 F3	H-P0264	ATP-dependent protease binding subunit (clpB)	94.27	
M365 G3	H-P0266	dihydroorotase (pyrC)	41.69	
M365 H3	H-P0267	chlorohydrolase	45.1	
M365 A4	H-P0271	hypothetical protein	36.08	
M365 B4	H-P0275	ATP-dependent nuclease (addB)	47.41	

M381 G3	H-P0276	hypothetical protein	20.46	
M365 C4	H-P0278	guanosine pentaphosphate phosphohydrolase (gppA)	53.35	
M365 D4	H-P0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	37.51	
M365 E4	H-P0280	heat shock protein B (ibpB)	36.19	
M365 F4	H-P0282	hypothetical protein	52.91	
M365 G4	H-P0283	3-dehydroquinate synthase (aroB)	37.84	
M365 H4	H-P0284	conserved hypothetical integral membrane protein	57.64	
M365 A5	H-P0285	conserved hypothetical protein	46.09	
M381 A4	H-P0287	hypothetical protein	19.03	
M381 C4	H-P0288	hypothetical protein	17.38	
M366 A1	H-P0389	superoxide dismutase (sodB)	23.54	
M366 B1	H-P0390	adhesin-thiol peroxidase (tagD)	18.37	
M366 C1	H-P0391	purine-binding chemotaxis protein (cheW)	18.26	
M366 D1	H-P0392	histidine kinase (cheA)	88.44	
M366 E1	H-P0393	chemotaxis protein (cheV)	34.32	
M366 F1	H-P0394	hypothetical protein	27.83	
M366 G1	H-P0395	conserved hypothetical protein	24.53	
M366 H1	H-P0396	conserved hypothetical protein	67.87	
M366 A2	H-P0397	phosphoglycerate dehydrogenase (serA)	57.75	
M366 B2	H-P0398	hypothetical protein	20.13	
M366 C2	H-P0399	ribosomal protein S1 (rps1)	61.27	
M366 D2	H-P0403	phenylalanyl-tRNA synthetase, alpha subunit (pheS)	36.19	
M366 E2	H-P0404	protein kinase C inhibitor (SP:P16436)	11.55	
M366 F2	H-P0405	nifS-like protein	48.51	
M366 G2	H-P0406	hypothetical protein	21.67	
M366 H2	H-P0407	biotin sulfoxide reductase (bisC)	87.67	
M381 D1	H-P0409	GMP synthase (guaA)	55.99	
M381 F1	H-P0410	putative neuraminylactose- binding hemagglutinin homolog (hpaA)	27.5	
M366 A3	H-P0411	hypothetical protein	11.66	
M366 B3	H-P0412	hypothetical protein	3.63	
M366 C3	H-P0413	transposase-like protein, PS3IS	29.59	
M366 D3	H-P0414	IS200 insertion sequence from SARA17	15.29	
M366 E3	H-P0415	conserved hypothetical integral membrane protein	68.64	
M366 F3	H-P0416	cyclopropane fatty acid synthase (cfa)	42.9	
M366 G3	H-P0417	methionyl-tRNA synthetase (metS)	71.61	
M366 H3	H-P0418	hypothetical protein	36.96	
M366 A4	H-P0419	conserved hypothetical protein	28.82	
M366 B4	H-P0420	hypothetical protein	15.73	
M366 C4	H-P0421	type I capsular polysaccharide biosynthesis protein J (capJ)	42.9	

M366 D4	H-P0422	arginine decarboxylase (speA)	67.76	
M366 E4	H-P0424	hypothetical protein	68.2	
M366 F4	H-P0425	hypothetical protein	45.98	
M366 G4	H-P0427	hypothetical protein	12.32	
M366 H4	H-P0433	hypothetical protein	16.28	
M366 A5	H-P0436	hypothetical protein	13.42	
M366 B5	H-P0437	IS605 transposase (tnpA)	15.73	
M366 C5	H-P0438	IS605 transposase (tnpB)	47.08	
M366 D5	H-P0442	hypothetical protein	9.79	
M366 E5	H-P0445	hypothetical protein	6.82	
M366 F5	H-P0452	hypothetical protein	57.09	
M366 G5	H-P0455	hypothetical protein	11.44	
M366 H5	H-P0457	hypothetical protein	9.68	
M366 A6	H-P0463	type I restriction enzyme M protein (hsdM)	53.68	
M366 B6	H-P0464	type I restriction enzyme R protein (hsdR)	116.16	
M366 C6	H-P0465	conserved hypothetical protein	69.52	
M366 D6	H-P0466	conserved hypothetical protein	28.16	
M366 E6	H-P0467	conserved hypothetical integral membrane protein	12.76	
M366 F6	H-P0468	conserved hypothetical protein	54.56	
M366 G6	H-P0469	conserved hypothetical protein	17.93	
M366 H6	H-P0471	glutathione-regulated potassium-efflux system protein (kefB)	45.87	
M366 A7	H-P0472	outer membrane protein (omp11)	20.57	
M366 B7	H-P0473	molybdenum ABC transporter, periplasmic molybdate-binding protein (modA)	27.17	
M366 C7	H-P0474	molybdenum ABC transporter, permease protein (modB)	24.75	
M366 D7	H-P0475	molybdenum ABC transporter, ATP-binding protein (modD)	29.26	
M366 E7	H-P0476	glutamyl-tRNA synthetase (gltX)	51.04	
M366 F7	H-P0477	outer membrane protein (omp12)	40.48	
M366 G7	H-P0478	adenine specific DNA methyltransferase (VSPIM)	60.06	
M366 H7	H-P0479	hypothetical protein	31.13	
M366 A8	H-P0481	adenine specific DNA methyltransferase (MFOKI)	23.32	
M366 B8	H-P0482	hypothetical protein	18.81	
M366 C8	H-P0483	cytosine specific DNA methyltransferase (H-PHMC)	36.3	
M367 A1	H-P0486	hypothetical protein	58.19	
M367 B1	H-P0487	hypothetical protein	52.91	
M367 C1	H-P0489	hypothetical protein	32.56	
M367 D1	H-P0490	putative potassium channel protein, putative	41.69	
M367 E1	H-P0491	ribosomal protein L28 (rpL28)	6.93	
M367 F1	H-P0492	hypothetical protein	30.69	
M367 G1	H-P0494	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	46.53	
M367 H1	H-P0495	hypothetical protein	9.57	

M367 A2	H-P0496	conserved hypothetical protein	14.74	
M367 B2	H-P0498	sodium- and chloride-dependent transporter	48.73	
M367 C2	H-P0499	phospholipase A1 precursor (DR-phospholipase A)	39.16	
M367 D2	H-P0500	DNA polymerase III beta-subunit (dnaN)	41.25	
M367 E2	H-P0501	DNA gyrase, sub B (gyrB)	85.14	
M367 F2	H-P0503	hypothetical protein	27.17	
M367 G2	H-P0504	hypothetical protein	5.5	
M367 H2	H-P0505	hypothetical protein	17.05	
M367 A3	H-P0507	conserved hypothetical protein	23.43	
M367 B3	H-P0509	glycolate oxidase subunit (glcD)	50.6	
M367 C3	H-P0510	dihydropicolinate reductase (dapB)	28.05	
M367 D3	H-P0512	glutamine synthetase (glnA)	53.02	
M367 E3	H-P0514	ribosomal protein L9 (rpl9)	16.61	
M367 F3	H-P0515	heat shock protein (hslV)	19.91	
M367 G3	H-P0516	heat shock protein (hslU) ORF1	48.84	
M367 H3	H-P0517	GTP-binding protein (era)	33.33	
M367 A4	H-P0519	conserved hypothetical protein	30.47	
M367 B4	H-P0520	cag pathogenicity island protein (cag1)	12.76	
M367 C4	H-P0522	cag pathogenicity island protein (cag3)	53.02	
M367 D4	H-P0523	cag pathogenicity island protein (cag4)	18.7	
M367 E4	H-P0525	virB11 homolog	36.41	
M367 F4	H-P0526	cag pathogenicity island protein (cag6)	22	
M367 G4	H-P0528	cag pathogenicity island protein (cag8)	57.53	
M379 H1	H-P0531-2	cag pathogenicity island protein (cag11)	24.09	
M367 H4	H-P0532	cag pathogenicity island protein (cag12)	30.91	
M367 A5	H-P0534	cag pathogenicity island protein (cag13)	21.67	
M367 B5	H-P0541	cag pathogenicity island protein (cag20)	40.81	
M367 C5	H-P0542	cag pathogenicity island protein (cag21)	15.73	
M367 D5	H-P0545	cag pathogenicity island protein (cag24)	22.88	
M367 E5	H-P0549	glutamate racemase (glr)	28.16	
M367 F5	H-P0550	transcription termination factor Rho (rho)	48.29	
M367 G5	H-P0551	ribosomal protein L31 (rpl31)	7.48	
M367 H5	H-P0552	conserved hypothetical protein	31.68	
M367 A6	H-P0553	conserved hypothetical protein	25.08	
M367 B6	H-P0554	hypothetical protein	35.42	
M367 C6	H-P0555	hypothetical protein	30.14	
M367 D6	H-P0556	hypothetical protein	16.06	

M367 E6	H-P0557	acetyl-coenzyme A carboxylase (accA)	34.43	
M367 F6	H-P0558	beta ketoacyl-acyl carrier protein synthase II (fabF)	45.43	
M367 G6	H-P0561	3-ketoacyl-acyl carrier protein reductase (fabG)	27.28	
M367 H6	H-P0562	ribosomal protein S21 (rps21)	7.81	
M367 A7	H-P0563	hypothetical protein	45.87	
M367 B7	H-P0566	diaminopimelate epimerase (dapF)	30.14	
M367 C7	H-P0568	hypothetical protein	28.16	
M367 D7	H-P0570	aminopeptidase a/i (pepA)	54.67	
M367 E7	H-P0571	conserved hypothetical integral membrane protein	21.23	
M379 A2	H-P0572-2	adenine phosphoribosyltransferase (apt)	19.8	
M379 B2	H-P0573-2	hypothetical protein	12.21	
M379 C2	H-P0574-2	galactosidase acetyltransferase (lacA)	16.72	
M379 D2	H-P0575-2	conserved hypothetical membrane protein	25.63	
M379 E2	H-P0576-2	signal peptidase I (lepB)	32.01	
M367 F7	H-P0577	methylene-tetrahydrofolate dehydrogenase (folD)	32.23	
M367 G7	H-P0579	hypothetical protein	20.35	
M367 H7	H-P0580	hypothetical protein	41.03	
M367 A8	H-P0581	dihydroorotase (pyrC)	37.4	
M367 B8	H-P0582	hypothetical protein	35.75	
M367 C8	H-P0583	hypothetical protein	32.34	
M368 A1	H-P0584	flagellar switch protein (fliN)	13.64	
M368 B1	H-P0585	endonuclease III (nth)	24.09	
M368 C1	H-P0587	aminodeoxychorismate lyase (pabC)	36.3	
M368 D1	H-P0591	ferredoxin oxidoreductase, gamma subunit	20.57	
M368 E1	H-P0593	adenine specific DNA methyltransferase (mod)	65.89	
M368 F1	H-P0594	hypothetical protein	6.05	
M368 G1	H-P0596	hypothetical protein	21.23	
M368 H1	H-P0597	penicillin-binding protein 1A (PBP-1A)	72.6	
M368 A2	H-P0599	hemolysin secretion protein precursor (hylB)	47.74	
M368 B2	H-P0601	flagellin A (flaA)	56.21	
M368 C2	H-P0602	endonuclease III	24.09	
M368 D2	H-P0603	hypothetical protein	20.9	
M379 F2	H-P0608-2	hypothetical protein	17.71	
M368 E2	H-P0614	hypothetical protein	12.32	
M368 F2	H-P0616	chemotaxis protein (cheV)	34.54	
M368 G2	H-P0617	aspartyl-tRNA synthetase (aspS)	63.58	
M368 H2	H-P0621	DNA mismatch repair protein (MutS)	83.93	
M368 A3	H-P0622	hypothetical protein	13.31	

M368 B3	H-P0623	UDP-N-acetylmuramate-alanine ligase (murC)	49.5	
M368 C3	H-P0625	protein E (gcpE)	39.6	
M368 D3	H-P0626	tetrahydrodipicolinate N-succinyltransferase (dapD)	44.22	
M368 E3	H-P0627	hypothetical protein	12.21	
M368 F3	H-P0629	hypothetical protein	75.02	
M368 G3	H-P0630	modulator of drug activity (mda66)	21.45	
M368 H3	H-P0631	quinone-reactive Ni/Fe hydrogenase, small subunit (hydA)	42.35	
M368 A4	H-P0632	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB)	63.69	
M368 B4	H-P0633	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit (hydC)	24.75	
M368 C4	H-P0634	quinone-reactive Ni/Fe hydrogenase (hydD)	19.69	
M368 D4	H-P0635	hypothetical protein	56.43	
M368 E4	H-P0636	hypothetical protein	10.23	
M368 F4	H-P0637	hypothetical protein	16.61	
M368 G4	H-P0638	outer membrane protein (omp13)	33.66	
M368 H4	H-P0643	glutamyl-tRNA synthetase (gltX)	48.4	
M368 A5	H-P0644	conserved hypothetical integral membrane protein	10.78	
M368 B5	H-P0645	soluble lytic murein transglycosylase (slt)	61.71	
M368 C5	H-P0646	UDP-glucose pyrophosphorylase (galU)	30.14	
M368 D5	H-P0647	hypothetical protein	14.96	
M368 E5	H-P0648	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	46.53	
M368 F5	H-P0649	aspartate ammonia-lyase (aspA)	51.59	
M368 G5	H-P0650	hypothetical protein	21.67	
M379 A3	H-P0651-2	fucosyltransferase	52.47	
M381 E3	H-P0652	phosphoserine phosphatase (serB)	22.88	
M368 H5	H-P0653	nonheme iron-containing ferritin (pfr)	18.48	
M379 G2	H-P0654-2	conserved hypothetical protein	39.71	
M379 H2	H-P0655-2	protective surface antigen D15	100.87	
M368 A6	H-P0656	conserved hypothetical protein	42.24	
M368 B6	H-P0657	processing protease (ymxG)	47.63	
M368 C6	H-P0658	PET112-like protein	52.36	
M368 D6	H-P0659	hypothetical protein	45.65	
M368 E6	H-P0660	hypothetical protein	37.29	
M368 F6	H-P0661	ribonuclease H (rmhA)	15.84	
M368 G6	H-P0662	ribonuclease III (rnc)	26.51	
M368 H6	H-P0663	chorismate synthase (aroC)	40.26	
M368 A7	H-P0665	oxygen-independent coproporphyrinogen III oxidase (hemN)	50.38	

M368 B7	H-P0667	hypothetical protein	9.46	
M368 C7	H-P0668	hypothetical protein	66.88	
M368 D7	H-P0671	outer membrane protein (omp14)	29.81	
M368 E7	H-P0672	solute-binding signature and mitochondrial signature protein (aspB)	43.01	
M379 B3	H-P0673-2	hypothetical protein	46.97	
M381 H3	H-P0674	hypothetical protein	25.19	
M368 F7	H-P0676	methylated-DNA-protein-cysteine methyltransferase (dat1)	18.59	
M368 G7	H-P0677	conserved hypothetical integral membrane protein	28.16	
M368 H7	H-P0679	lipopolysaccharide biosynthesis protein (wbpB)	31.9	
M369 A1	H-P0681	hypothetical protein	18.59	
M369 B1	H-P0682	hypothetical protein	13.97	
M369 C1	H-P0683	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	47.74	
M369 D1	H-P0685	flagellar biosynthetic protein (fliP)	19.03	
M369 E1	H-P0687	iron(II) transport protein (feoB)	70.73	
M369 F1	H-P0688	hypothetical protein	18.37	
M369 G1	H-P0690	acetyl coenzyme A acetyltransferase (thiolase) (fadA)	43.12	
M381 A1	H-P0691	3-oxoadipate coA-transferase subunit A (yxjD)	25.63	
M381 B1	H-P0692	3-oxoadipate coA-transferase subunit B (yxjE)	22.88	
M369 H1	H-P0694	hypothetical protein	28.38	
M369 A2	H-P0695	hydantoin utilization protein A (hyuA)	78.54	
M369 B2	H-P0697	hypothetical protein	18.59	
M369 C2	H-P0699	hypothetical protein	37.73	
M369 D2	H-P0700	diacylglycerol kinase (dgkA)	14.19	
M369 E2	H-P0701	DNA gyrase, sub A (gyrA)	91.08	
M369 F2	H-P0703	response regulator	42.02	
M369 G2	H-P0707	conserved hypothetical protein	33.99	
M369 H2	H-P0711	hypothetical protein	44.77	
M369 A3	H-P0715	ABC transporter, ATP-binding protein	26.51	
M369 B3	H-P0716	conserved hypothetical protein	14.74	
M369 C3	H-P0718	conserved hypothetical integral membrane protein	23.21	
M369 D3	H-P0719	hypothetical protein	12.1	
M369 E3	H-P0723	L-asparaginase II (ansB)	36.41	
M369 F3	H-P0724	anaerobic C4-dicarboxylate transport protein (dcuA)	48.84	
M369 G3	H-P0727	transcriptional regulator, putative	36.19	
M369 H3	H-P0728	conserved hypothetical protein	37.07	
M369 A4	H-P0730	hypothetical protein	11.22	
M369 B4	H-P0732	hypothetical protein	13.09	
M369 C4	H-P0734	conserved hypothetical protein	48.4	

M369 D4	H-P0735	xanthine guanine phosphoribosyl transferase (gpt)	16.94	
M369 E4	H-P0737	conserved hypothetical integral membrane protein	17.49	
M381 H2	H-P0738	D-alanine:D-alanine ligase A (ddlA)	38.28	
M369 F4	H-P0739	2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	26.62	
M369 G4	H-P0741	conserved hypothetical protein	17.82	
M369 H4	H-P0745	conserved hypothetical protein	36.08	
M369 A5	H-P0747	conserved hypothetical protein	43.34	
M369 B5	H-P0748	cell division protein (ftsE)	24.64	
M369 C5	H-P0749	cell division membrane protein (ftsX)	29.59	
M369 D5	H-P0750	hypothetical protein	44.11	
M369 E5	H-P0752	flagellar hook-associated protein 2 (fliD)	74.25	
M381 F3	H-P0755	molybdopterin biosynthesis protein (moeB)	23.21	
M379 C3	H-P0757-2	beta-alanine synthetase homolog	32.23	
M369 F5	H-P0758	conserved hypothetical integral membrane protein	48.18	
M369 G5	H-P0759	conserved hypothetical integral membrane protein	45.98	
M369 H5	H-P0761	hypothetical protein	22.11	
M369 A6	H-P0762	hypothetical protein	20.46	
M369 B6	H-P0767	hypothetical protein	2.75	
M369 C6	H-P0768	molybdenum cofactor biosynthesis protein A (moaA)	35.42	
M369 D6	H-P0769	molybdopterin-guanine dinucleotide biosynthesis protein A (mobA)	22.22	
M369 E6	H-P0771	hypothetical protein	27.06	
M369 F6	H-P0772	N-acetylmuramoyl-L-alanine amidase (amiA)	48.51	
M369 G6	H-P0773	hypothetical protein	40.04	
M369 H6	H-P0777	uridine 5'-monophosphate (UMP) kinase (pyrH)	26.51	
M370 A1	H-P0782	hypothetical protein	50.16	
M370 B1	H-P0783	hypothetical protein	18.26	
M370 C1	H-P0792	sigma-54 interacting protein	55.77	
M370 D1	H-P0793	polypeptide deformylase (def)	19.25	
M370 E1	H-P0794	ATP-dependent clp protease proteolytic component (clpP)	21.67	
M370 F1	H-P0796	outer membrane protein (omp18)	30.69	
M379 G3	H-P0797-2	flagellar sheath adhesin hpaA	28.71	
M379 H3	H-P0798-2	molybdenum cofactor biosynthesis protein C (moaC)	17.49	
M370 G1	H-P0799	molybdopterin biosynthesis protein (mog)	19.47	
M370 H1	H-P0800	molybdopterin converting factor, subunit 2 (moaE)	16.06	

M379 A4	H-P0801-2	molybdopterin converting factor, subunit I (moaD)	8.25	
M379 B4	H-P0802-2	GTP cyclohydrolase II (ribA)	21.23	
M379 D3	H-P0803-2	hypothetical protein	30.8	
M379 E3	H-P0804-2	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase (ribA, ribB)	37.95	
M379 F3	H-P0805-2	lipooligosaccharide 5G8 epitope biosynthesis-associated protein (lex2B)	31.35	
M370 A2	H-P0806	hypothetical protein	22.77	
M379 C4	H-P0807-2	iron(III) dicitrate transport protein (fecA)	86.68	
M370 B2	H-P0808	holo-acp synthase (acpS)	13.2	
M370 C2	H-P0809	hypothetical protein	20.24	
M370 D2	H-P0810	conserved hypothetical protein	22.11	
M370 E2	H-P0811	hypothetical protein	11.99	
M370 F2	H-P0812	hypothetical protein	37.07	
M370 G2	H-P0813	conserved hypothetical protein	22.66	
M370 H2	H-P0814	thiamin biosynthesis protein (thiF)	28.16	
M370 A3	H-P0815	flagellar motor rotation protein (motA)	28.38	
M370 B3	H-P0831	conserved hypothetical ATP binding protein	21.67	
M379 D4	H-P0832-2	spermidine synthase (speE)	28.93	
M379 E4	H-P0833-2	hypothetical protein	32.23	
M370 C3	H-P0834	GTP-binding protein homologue (yphC)	50.49	
M370 D3	H-P0835	histone-like DNA-binding protein HU (hup)	10.45	
M370 E3	H-P0836	hypothetical protein	13.2	
M370 F3	H-P0837	hypothetical protein	11.33	
M370 G3	H-P0838	hypothetical protein	22.66	
M370 H3	H-P0839	outer membrane protein P1 (ompP1)	64.68	
M370 A4	H-P0840	flaA1 protein	36.74	
M370 B4	H-P0841	pantothenate metabolism flavoprotein (dfp)	46.86	
M370 C4	H-P0843	thiamin phosphate pyrophosphorylase/hydroxyethylthiazole kinase (thiB)	24.2	
M370 D4	H-P0845	thiamin phosphate pyrophosphorylase/hydroxyethylthiazole kinase (thiM)	30.14	
M370 E4	H-P0850	type I restriction enzyme M protein (hsdM)	58.08	
M370 F4	H-P0851	conserved hypothetical integral membrane protein	25.08	
M370 G4	H-P0854	GMP reductase (guaC)	36.08	
M370 H4	H-P0858	ADP-heptose synthase (rfaE)	50.82	
M370 A5	H-P0859	ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD)	36.41	

M370 B5	H-P0861	hypothetical protein	27.17	
M370 C5	H-P0862	hypothetical protein	24.64	
M379 F4	H-P0863-2	hypothetical protein	59.73	
M370 D5	H-P0865	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	16.06	
M370 E5	H-P0866	transcription elongation factor GreA (greA)	18.15	
M379 G4	H-P0867-2	lipid A disaccharide synthetase (lpxB)	39.71	
M379 H4	H-P0870-2	flagellar hook (flgE)	79.09	
M370 F5	H-P0871	CDP-diglyceride hydrolase (cdh)	26.95	
M370 G5	H-P0872	alkylphosphonate uptake protein (phnA)	12.1	
M370 H5	H-P0873	hypothetical protein	7.92	
M371 A1	H-P0879	hypothetical protein	22.33	
M371 B1	H-P0883	Holliday junction DNA helicase (ruvA)	20.24	
M371 C1	H-P0885	virulence factor mviN protein (mviN)	50.82	
M371 D1	H-P0886	cysteinyl-tRNA synthetase (cysS)	51.26	
M371 E1	H-P0889	iron(III) dicitrate ABC transporter, permease protein (fecD)	35.97	
M371 F1	H-P0890	conserved hypothetical protein	28.27	
M371 G1	H-P0891	conserved hypothetical protein	19.25	
M371 H1	H-P0892	conserved hypothetical protein	10.01	
M371 A2	H-P0894	conserved hypothetical protein	9.79	
M371 B2	H-P0895	hypothetical protein	13.86	
M371 C2	H-P0896	outer membrane protein (omp19)	77.99	
M371 D2	H-P0897	hypothetical protein	22.99	
M371 E2	H-P0898	hydrogenase expression/formation protein (hypD)	40.81	
M371 F2	H-P0899	hydrogenase expression/formation protein (hypC)	8.58	
M371 G2	H-P0900	hydrogenase expression/formation protein (hypB)	26.73	
M371 H2	H-P0905	phosphotransacetylase (pta)	24.64	
M371 A3	H-P0906	hypothetical protein	58.08	
M371 B3	H-P0907	hook assembly protein, flagella (flgD)	33.22	
M371 C3	H-P0909	hypothetical protein	22.22	
M371 D3	H-P0912	outer membrane protein (omp20)	56.76	
M371 E3	H-P0913	outer membrane protein (omp21)	58.3	
M371 F3	H-P0914	hypothetical protein	56.65	
M371 G3	H-P0915	iron-regulated outer membrane protein (frpB)	61.93	
M371 H3	H-P0916	iron-regulated outer membrane protein (frpB)	27.5	
M380 A1	H-P0917-2	hypothetical protein	2.64	
M371 A4	H-P0918	hypothetical protein	15.84	
M371 B4	H-P0920	conserved hypothetical integral membrane protein	25.41	

M371 C4	H-P0921	glyceraldehyde-3-phosphate dehydrogenase (gap)	36.63	
M371 D4	H-P0923	outer membrane protein (omp22)	40.7	
M371 E4	H-P0925	recombinational DNA repair protein (recR)	21.34	
M371 F4	H-P0927	heat shock protein (htpX)	35.97	
M371 G4	H-P0928	GTP cyclohydrolase I (folE)	19.91	
M371 H4	H-P0929	geranyltranstransferase (ispA)	33.44	
M371 A5	H-P0930	stationary-phase survival protein (surE)	29.48	
M371 B5	H-P0931	hypothetical protein	16.17	
M371 C5	H-P0932	hypothetical protein	11.11	
M371 D5	H-P0933	hypothetical protein	22.11	
M371 E5	H-P0934	conserved hypothetical protein	27.72	
M371 F5	H-P0935	hypothetical protein	17.82	
M371 G5	H-P0936	proline/betaine transporter (proP)	42.9	
M371 H5	H-P0938	hypothetical protein	12.76	
M371 A6	H-P0939	amino acid ABC transporter, permease protein (yckJ)	26.18	
M371 B6	H-P0940	amino acid ABC transporter, periplasmic binding protein (yckK)	28.27	
M371 C6	H-P0941	alanine racemase, biosynthetic (alr)	41.58	
M371 D6	H-P0942	D-alanine glycine permease (dagA)	49.61	
M371 E6	H-P0943	D-amino acid dehydrogenase (dadA)	45.21	
M371 F6	H-P0944	translation initiation inhibitor, putative	13.86	
M371 G6	H-P0946	conserved hypothetical integral membrane protein	54.67	
M371 H6	H-P0947	hypothetical protein	13.31	
M371 A7	H-P0949	conserved hypothetical secreted protein	16.61	
M371 B7	H-P0950	acetyl-CoA carboxylase beta subunit (accD)	31.9	
M371 C7	H-P0951	hypothetical protein	22.66	
M371 D7	H-P0952	conserved hypothetical integral membrane protein	24.09	
M371 E7	H-P0953	hypothetical protein	20.79	
M371 F7	H-P0955	prolipoprotein diacylglycerol transferase (lgt)	31.35	
M371 G7	H-P0956	conserved hypothetical protein	26.73	
M371 H7	H-P0957	3-deoxy-d-manno-octulosonic-acid transferase (kdtA)	43.34	
M371 A8	H-P0958	hypothetical protein	28.05	
M371 B8	H-P0960	glycyl-tRNA synthetase, alpha subunit (glyQ)	33.44	
M371 C8	H-P0961	glycerol-3-phosphate dehydrogenase (NAD(P)+)	34.43	
M380 B1	H-P0965-2	hypothetical protein	48.84	
M371 D8	H-P0966	conserved hypothetical protein	60.5	

M380 F1	H-P0968-2	hypothetical protein	2.42	
M371 E8	H-P0969	cation efflux system protein (czcA)	112.31	
M371 F8	H-P0970	nickel-cobalt-cadmium resistance protein (nccB)	39.6	
M371 G8	H-P0971	hypothetical protein	45.54	
M371 H8	H-P0972	glycyl-tRNA synthetase, beta subunit (glyS)	77.22	
M371 A9	H-P0973	hypothetical protein	38.94	
M380 C1	H-P0974-2	phosphoglycerate mutase (pgm)	54.12	
M380 D1	H-P0975-2	conserved hypothetical protein	10.34	
M380 E1	H-P0976-2	adenosylmethionine-8-amino-7-oxononanoate aminotransferase (bioA)	48.07	
M380 H1	H-P0994-2	hypothetical protein	29.48	
M380 G1	H-P1000-2	PARA protein	24.09	
M380 A2	H-P1001-2	hypothetical protein	10.45	
M380 B2	H-P1002-2	hypothetical protein	43.45	
M380 C2	H-P1003-2	hypothetical protein	40.81	
M380 D2	H-P1004-2	hypothetical protein	30.14	
M380 E2	H-P1005-2	hypothetical protein	11.55	
M380 F2	H-P1006-2	conjugal transfer protein (traG)	19.58	
M380 G2	H-P1017-2	amino acid permease (rocE)	57.2	
M380 H2	H-P1042-2	hypothetical protein	38.39	
M380 A3	H-P1056-2	hypothetical protein	31.35	
M380 B3	H-P1075-2	conserved hypothetical secreted protein	48.29	
M373 A1	H-P1076	hypothetical protein	18.92	
M373 B1	H-P1077	nickel transport protein (nixA)	36.52	
M373 C1	H-P1080	conserved hypothetical integral membrane protein	20.9	
M373 D1	H-P1081	hypothetical protein	22.88	
M373 E1	H-P1082	multidrug resistance protein (msbA)	60.72	
M373 F1	H-P1083	hypothetical protein	52.8	
M373 G1	H-P1084	aspartate transcarbamoylase (pyrB)	33.88	
M373 H1	H-P1085	hypothetical protein	18.92	
M373 A2	H-P1086	hemolysin (tly)	25.96	
M373 B2	H-P1087	riboflavin biosynthesis regulatory protein (ribC)	30.91	
M373 C2	H-P1088	transketolase A (tktA)	70.62	
M373 D2	H-P1091	alpha-ketoglutarate permease (kgtP)	46.97	
M373 E2	H-P1092	flagellar basal-body rod protein (flgG)	29.7	
M373 F2	H-P1096	IS605 transposase (tnpA)	15.73	
M373 G2	H-P1098	conserved hypothetical secreted protein	32.01	
M373 H2	H-P1101	glucose-6-phosphate dehydrogenase (g6pD)	46.86	
M373 A3	H-P1102	glucose-6-phosphate 1-dehydrogenase (devB)	25.08	

M373 B3	H-P1103	glucokinase (glk)	37.07	
M373 C3	H-P1108	pyruvate ferredoxin oxidoreductase, gamma subunit	20.57	
M373 D3	H-P1109	pyruvate ferredoxin oxidoreductase, delta subunit	14.41	
M373 E3	H-P1110	pyruvate ferredoxin oxidoreductase, alpha subunit	44.88	
M373 F3	H-P1111	pyruvate ferredoxin oxidoreductase, beta subunit	34.65	
M373 G3	H-P1112	adenylosuccinate lyase (purB)	48.51	
M380 C3	H-P1113-2	outer membrane protein (omp24)	30.58	
M373 H3	H-P1117	conserved hypothetical secreted protein	28.27	
M373 A4	H-P1120	hypothetical protein	15.95	
M373 B4	H-P1121	cytosine specific DNA methyltransferase (BSP6IM)	34.43	
M380 D3	H-P1122-2	hypothetical protein	8.47	
M373 C4	H-P1123	peptidyl-prolyl cis-trans isomerase, FKBP-type rotamase (slyD)	20.46	
M373 D4	H-P1124	hypothetical protein	36.52	
M373 E4	H-P1125	peptidoglycan associated lipoprotein precursor (omp18)	19.8	
M373 F4	H-P1126	colicin tolerance-like protein (tolB)	45.98	
M373 G4	H-P1128	hypothetical protein	9.35	
M373 H4	H-P1129	biopolymer transport protein (exbD)	14.74	
M373 A5	H-P1131	ATP synthase F1, subunit epsilon (atpC)	13.75	
M373 B5	H-P1134	ATP synthase F1, subunit alpha (atpA)	55.44	
M373 C5	H-P1135	ATP synthase F1, subunit delta (atpH)	19.91	
M373 D5	H-P1137	ATP synthase F0, subunit b' (atpF')	15.95	
M373 E5	H-P1138	plasmid replication-partition related protein	32.01	
M373 F5	H-P1139	SpoOJ regulator (soj)	29.15	
M373 G5	H-P1140	biotin operon repressor/biotin acetyl coenzyme A carboxylase synthetase (birA)	23.43	
M373 H5	H-P1141	methionyl-tRNA formyltransferase (fmt)	33.44	
M373 A6	H-P1144	hypothetical protein	9.46	
M373 B6	H-P1145	hypothetical protein	11.44	
M373 C6	H-P1147	ribosomal protein L19 (rpl19)	13.09	
M373 D6	H-P1148	tRNA (guanine-N1)- methyltransferase (trmD)	25.3	
M373 E6	H-P1149	conserved hypothetical protein	20.35	
M380 F3	H-P1150-2	hypothetical protein	12.76	
M373 F6	H-P1152	signal recognition particle protein (ffh)	49.39	

M380 G3	H-P1153-2	valyl-tRNA synthetase (valS)	96.25	
M380 E3	H-P1157-2	outer membrane protein (omp26)	135.41	
M373 G6	H-P1158	pyrroline-5-carboxylate reductase (proC)	28.38	
M373 H6	H-P1159	cell filamentation protein (fic)	19.58	
M373 A7	H-P1160	conserved hypothetical protein	15.51	
M380 A4	H-P1163-2	hypothetical protein	7.04	
M373 B7	H-P1165	tetracycline resistance protein tetA(P), putative	42.57	
M373 C7	H-P1168	carbon starvation protein (cstA)	75.68	
M373 D7	H-P1169	glutamine ABC transporter, permease protein (glnP)	23.98	
M380 H3	H-P1169-2	glutamine ABC transporter, permease protein (glnP)	23.98	
M374 A1	H-P1170	glutamine ABC transporter, permease protein (glnP)	24.64	
M374 B1	H-P1171	glutamine ABC transporter, ATP-binding protein (glnQ)	27.39	
M374 C1	H-P1172	glutamine ABC transporter, periplasmic glutamine-binding protein (glnH)	30.58	
M374 D1	H-P1173	hypothetical protein	20.24	
M374 E1	H-P1174	glucose/galactose transporter (gluP)	44.88	
M374 F1	H-P1175	conserved hypothetical integral membrane protein	47.96	
M374 G1	H-P1177	outer membrane protein (omp27)	70.62	
M374 H1	H-P1178	purine-nucleoside phosphorylase (deoD)	25.74	
M374 A2	H-P1179	phosphopentomutase (deoB)	45.54	
M374 B2	H-P1180	pyrimidine nucleoside transport protein (nupC)	46.09	
M374 C2	H-P1183	NA ⁺ /H ⁺ antiporter (napA)	42.24	
M374 D2	H-P1184	conserved hypothetical integral membrane protein	50.6	
M374 E2	H-P1185	conserved hypothetical integral membrane protein	43.12	
M374 F2	H-P1186	carbonic anhydrase	22.33	
M374 G2	H-P1187	hypothetical protein	42.46	
M374 H2	H-P1188	hypothetical protein	29.7	
M374 A3	H-P1189	aspartate-semialdehyde dehydrogenase (asd)	38.17	
M374 B3	H-P1191	ADP-heptose-lps heptosyltransferase II (rfaF)	38.5	
M374 C3	H-P1196	ribosomal protein S7 (rps7)	17.16	
M374 D3	H-P1200	ribosomal protein L10 (rpl10)	18.15	
M374 E3	H-P1201	ribosomal protein L1 (rpl1)	25.85	
M374 F3	H-P1202	ribosomal protein L11 (rpl11)	15.62	
M374 G3	H-P1203	transcription termination factor NusG (nusG)	19.47	
M380 B4	H-P1205-2	translation elongation factor EF-Tu (tufB)	44	

M374 H3	H-P1206	multidrug resistance protein (hetA)	63.69	
M374 A4	H-P1207	hypothetical protein	24.53	
M374 B4	H-P1210	serine acetyltransferase (cysE)	18.92	
M380 F4	H-P1213-2	polynucleotide phosphorylase (pnp)	75.79	
M380 G4	H-P1214-2	conserved hypothetical protein	26.51	
M380 C4	H-P1215-2	hypothetical protein	8.91	
M380 D4	H-P1216-2	conserved hypothetical secreted protein	72.71	
M380 E4	H-P1217-2	hypothetical protein	17.6	
M374 C4	H-P1220	ABC transporter, ATP-binding protein (yhcG)	25.19	
M374 D4	H-P1221	conserved hypothetical protein	25.85	
M374 E4	H-P1222	D-lactate dehydrogenase (dld)	104.39	
M374 F4	H-P1224	uroporphyrinogen III cosynthase (hemD)	24.97	
M374 G4	H-P1225	conserved hypothetical integral membrane protein	14.41	
M374 H4	H-P1226	oxygen-independent coproporphyrinogen III oxidase (hemN)	38.83	
M380 H4	H-P1227-2	cytochrome c553	10.67	
M380 A5	H-P1228-2	invasion protein (invA)	17.16	
M380 B5	H-P1229-2	aspartokinase (lysC)	44.66	
M374 A5	H-P1230	hypothetical protein	19.91	
M374 B5	H-P1231	DNA polymerase III delta prime subunit (holB)	24.09	
M374 C5	H-P1232	dihydropteroate synthase (folP)	41.91	
M380 D5	H-P1233-2	hypothetical protein	16.94	
M374 D5	H-P1234	conserved hypothetical integral membrane protein	32.89	
M374 E5	H-P1235	conserved hypothetical integral membrane protein	45.76	
M374 F5	H-P1236	hypothetical protein	20.24	
M374 G5	H-P1237	carbamoyl-phosphate synthetase (pyrAa)	41.36	
M374 H5	H-P1240	conserved hypothetical protein	21.01	
M380 C5	H-P1241-2	alanyl-tRNA synthetase (alaS)	93.28	
M374 A6	H-P1242	conserved hypothetical protein	8.47	
M380 H5	H-P1243-2	outer membrane protein (omp28)	80.74	
M374 B6	H-P1244	ribosomal protein S18 (rps18)	9.46	
M374 C6	H-P1245	single-strand DNA-binding protein (ssb)	19.8	
M374 D6	H-P1246	ribosomal protein S6 (rps6)	15.73	
M380 A6	H-P1247-2	hypothetical protein	37.51	
M374 E6	H-P1248	virulence associated protein homolog (vacB)	70.95	
M380 B6	H-P1249-2	shikimate 5-dehydrogenase (aroE)	29.04	
M380 E5	H-P1251-2	oligopeptide ABC transporter, permease protein (oppB)	38.39	

M380 F5	H-P1252-2	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA)	65.45	
M380 G5	H-P1253-2	tryptophanyl-tRNA synthetase (trpS)	37.4	
M374 F6	H-P1254	biotin synthesis protein (bioC)	26.51	
M374 G6	H-P1255	protein translocation protein, low temperature (secG)	22.22	
M374 H6	H-P1256	ribosome releasing factor (frr)	20.46	
M374 A7	H-P1257	orotate phosphoribosyltransferase (pyrE)	22.22	
M374 B7	H-P1258	conserved hypothetical mitochondrial protein 4	17.05	
M374 C7	H-P1260	NADH-ubiquinone oxidoreductase, NQO7 subunit (NQO7)	14.74	
M374 D7	H-P1262	NADH-ubiquinone oxidoreductase, NQO5 subunit (NQO5)	29.37	
M374 E7	H-P1263	NADH-ubiquinone oxidoreductase, NQO4 subunit (NQO4)	45.1	
M380 C6	H-P1264-2	hypothetical protein	8.47	
M374 F7	H-P1265	hypothetical protein	36.19	
M375 A1	H-P1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	24.31	
M375 B1	H-P1275	phosphomannomutase (algC)	50.6	
M375 C1	H-P1277	tryptophan synthase, alpha subunit (trpA)	28.93	
M375 D1	H-P1278	tryptophan synthase, beta subunit (trpB)	43.34	
M375 E1	H-P1279	anthranilate isomerase (trpC)	49.83	
M375 F1	H-P1282	anthranilate synthase component I (trpE)	55.11	
M375 G1	H-P1285	conserved hypothetical secreted protein	25.41	
M375 H1	H-P1286	conserved hypothetical secreted protein	20.13	
M375 A2	H-P1287	transcriptional regulator (tenA)	23.98	
M375 B2	H-P1288	hypothetical protein	14.63	
M375 C2	H-P1289	hypothetical protein	17.82	
M375 D2	H-P1290	nicotinamide mononucleotide transporter (pnuC)	24.31	
M375 E2	H-P1291	conserved hypothetical protein	22.55	
M375 F2	H-P1292	ribosomal protein L17 (rpl17)	12.87	
M375 G2	H-P1293	DNA-directed RNA polymerase, alpha subunit (rpoA)	37.95	
M375 H2	H-P1294	ribosomal protein S4 (rps4)	22.99	
M375 A3	H-P1295	ribosomal protein S11 (rps11)	14.52	
M375 B3	H-P1296	ribosomal protein S13 (rps13)	13.31	
M380 D6	H-P1298-2	translation initiation factor EF-1 (infA)	8.03	

M375 C3	H-P1299	methionine amino peptidase (map)	27.94	
M375 D3	H-P1302	ribosomal protein S5 (rps5)	16.94	
M375 E3	H-P1303	ribosomal protein L18 (rpl18)	13.2	
M375 F3	H-P1305	ribosomal protein S8 (rps8)	14.52	
M375 G3	H-P1307	ribosomal protein L5 (rpl5)	20.02	
M375 H3	H-P1308	ribosomal protein L24 (rpl24)	8.14	
M375 A4	H-P1309	ribosomal protein L14 (rpl14)	13.53	
M375 B4	H-P1310	ribosomal protein S17 (rps17)	9.57	
M375 C4	H-P1312	ribosomal protein L16 (rpl16)	15.62	
M375 D4	H-P1314	ribosomal protein L22 (rpl22)	13.53	
M375 E4	H-P1315	ribosomal protein S19 (rps19)	10.34	
M375 F4	H-P1318	ribosomal protein L4 (rpl4)	23.76	
M375 G4	H-P1319	ribosomal protein L3 (rpl3)	21.12	
M375 H4	H-P1320	ribosomal protein S10 (rps10)	11.55	
M375 A5	H-P1321	conserved hypothetical ATP-binding protein	41.58	
M375 B5	H-P1322	hypothetical protein	22.22	
M375 C5	H-P1323	ribonuclease HII (rnhB)	23.1	
M375 D5	H-P1324	hypothetical protein	9.24	
M375 E5	H-P1326	hypothetical protein	13.86	
M375 F5	H-P1327	hypothetical protein	45.43	
M375 G5	H-P1328	cation efflux system protein (czcA)	37.29	
M375 H5	H-P1330	conserved hypothetical integral membrane protein	12.76	
M375 A6	H-P1331	conserved hypothetical integral membrane protein	25.19	
M375 B6	H-P1332	co-chaperone and heat shock protein (dnaJ)	40.7	
M375 C6	H-P1333	hypothetical protein	42.13	
M375 D6	H-P1335	conserved hypothetical protein	39.71	
M375 E6	H-P1336	hypothetical protein	27.94	
M375 F6	H-P1337	conserved hypothetical protein	19.25	
M375 G6	H-P1338	conserved hypothetical protein	16.39	
M375 H6	H-P1340	biopolymer transport protein (exbD)	14.3	
M375 A7	H-P1341	siderophore-mediated iron transport protein (tonB)	31.46	
M375 B7	H-P1342	outer membrane protein (omp29)	76.12	
M375 C7	H-P1343	conserved hypothetical integral membrane protein	26.73	
M375 D7	H-P1344	magnesium and cobalt transport protein (corA)	35.09	
M375 E7	H-P1345	phosphoglycerate kinase	44.33	
M375 F7	H-P1346	glyceraldehyde-3-phosphate dehydrogenase (gap)	36.41	
M375 G7	H-P1347	uracil-DNA glycosylase (ung)	25.74	
M375 H7	H-P1349	hypothetical protein	42.68	
M375 A8	H-P1350	protease	50.6	
M375 B8	H-P1355	nicotinate-nucleotide pyrophosphorylase (nadC)	30.14	
M375 C8	H-P1356	quinolinate synthetase A (nadA)	37.07	

M375 D8	H-P1357	phosphatidylserine decarboxylase proenzyme (psd)	29.48	
M375 E8	H-P1358	hypothetical protein	18.59	
M375 F8	H-P1360	4-hydroxybenzoate octaprenyltransferase (ubiA)	32.45	
M375 G8	H-P1361	competence locus E (comE3)	45.98	
M375 H8	H-P1362	replicative DNA helicase (dnaB)	53.79	
M375 A9	H-P1363	conserved hypothetical integral membrane protein	51.37	
M376 A1	H-P1364	signal-transducing protein, histidine kinase	43.78	
M376 B1	H-P1365	response regulator	23.54	
M376 C1	H-P1371	type III restriction enzyme R protein	106.59	
M376 D1	H-P1372	rod shape-determining protein (mreC)	27.39	
M376 E1	H-P1373	rod shape-determining protein (mreB)	38.28	
M376 F1	H-P1374	ATP-dependent protease ATPase subunit (clpX)	49.17	
M376 G1	H-P1375	UDP-N-acetylglucosamine acyltransferase (lpxA)	29.81	
M376 H1	H-P1376	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (fabZ)	17.6	
M376 A2	H-P1377	hypothetical protein	16.17	
M376 B2	H-P1378	competence lipoprotein (comL)	24.31	
M376 C2	H-P1379	ATP-dependent protease (lon)	91.96	
M376 D2	H-P1380	prephenate dehydrogenase (tyrA)	29.26	
M381 C1	H-P1381	hypothetical protein	8.58	
M376 E2	H-P1382	hypothetical protein	14.41	
M376 F2	H-P1383	restriction modification system S subunit	17.71	
M376 G2	H-P1384	hypothetical protein	7.59	
M376 H2	H-P1385	fructose-1,6-bisphosphatase	32.01	
M376 A3	H-P1386	D-ribulose-5-phosphate 3 epimerase (rpe)	23.98	
M376 B3	H-P1388	hypothetical protein	16.5	
M376 C3	H-P1389	hypothetical protein	6.71	
M376 D3	H-P1390	hypothetical protein	18.37	
M376 E3	H-P1391	hypothetical protein	10.89	
M376 F3	H-P1392	fibronectin/fibrinogen-binding protein	47.96	
M376 G3	H-P1393	DNA repair protein (recN)	57.75	
M376 H3	H-P1394	conserved hypothetical protein	31.35	
M376 A4	H-P1395	outer membrane protein (omp30)	26.73	
M376 B4	H-P1396	hypothetical protein	31.79	
M376 C4	H-P1398	alanine dehydrogenase (ald)	41.91	
M376 D4	H-P1399	arginase (rocF)	35.53	
M376 E4	H-P1400	iron(III) dicitrate transport protein (fecA)	92.73	
M376 F4	H-P1401	conserved hypothetical protein	25.96	

M381 A2	H-P1402	type I restriction enzyme R protein (hsdR)	109.34	
M381 B2	H-P1403	type I restriction enzyme M protein (hsdM)	89.98	
M376 G4	H-P1405	hypothetical protein	3.85	
M376 H4	H-P1406	biotin synthetase (bioB)	31.13	
M376 A5	H-P1407	conserved hypothetical integral membrane protein	32.23	
M381 C2	H-P1408	hypothetical protein	12.32	
M381 D2	H-P1409	hypothetical protein	63.69	
M376 B5	H-P1410	hypothetical protein	43.45	
M376 C5	H-P1411	hypothetical protein	68.2	
M376 D5	H-P1412	hypothetical protein	33.99	
M376 E5	H-P1413	conserved hypothetical protein	16.39	
M376 F5	H-P1414	conserved hypothetical protein	12.54	
M376 G5	H-P1415	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)	29.37	
M376 H5	H-P1418	UDP-N-acetylenolpyruvoylglucosamine reductase (murB)	28.6	
M376 A6	H-P1419	flagellar biosynthetic protein (fliQ)	9.79	
M376 B6	H-P1420	flagellar export protein ATP synthase (fliI)	47.85	
M376 C6	H-P1421	conjugative transfer regulon protein (trbB)	33.55	
M376 D6	H-P1423	conserved hypothetical protein	9.35	
M376 E6	H-P1424	hypothetical protein	22.77	
M376 F6	H-P1425	hypothetical protein	8.36	
M376 G6	H-P1427	histidine-rich, metal binding polypeptide (hpn)	6.71	
M376 H6	H-P1428	conserved hypothetical protein	39.38	
M376 A7	H-P1429	polysialic acid capsule expression protein (kpsF)	36.3	
M376 B7	H-P1430	conserved hypothetical ATP-binding protein	75.9	
M376 C7	H-P1431	16S rRNA (adenosine-N6,N6)-dimethyltransferase (ksgA)	29.92	
M376 D7	H-P1432	histidine and glutamine-rich protein	8.03	
M376 E7	H-P1433	hypothetical protein	94.27	
M376 F7	H-P1434	formyltetrahydrofolate hydrolase (purU)	32.34	
M376 G7	H-P1435	protease IV (PspA)	32.23	
M376 H7	H-P1436	hypothetical protein	9.13	
M376 A8	H-P1438	conserved hypothetical lipoprotein	37.29	
M376 B8	H-P1439	hypothetical protein	9.02	
M376 C8	H-P1440	hypothetical protein	28.6	
M376 D8	H-P1441	peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi)	18.04	

M376 E8	H-P1442	carbon storage regulator (csrA)	8.47	
M376 F8	H-P1443	conserved hypothetical protein	29.59	
M376 G8	H-P1444	small protein (smpB)	16.83	
M376 H8	H-P1445	biopolymer transport protein (exbB)	16.61	
M376 A9	H-P1446	biopolymer transport protein (exbD)	14.74	
M376 B9	H-P1447	ribosomal protein L34 (rpl34)	4.95	
M376 C9	H-P1448	ribonuclease P, protein component (mpA)	17.82	
M376 D9	H-P1449	conserved hypothetical protein	12.98	
M376 E9	H-P1450	60 kDa inner-membrane protein	60.28	
M376 F9	H-P1451	hypothetical protein	29.15	
M376 G9	H-P1452	thiophene and furan oxidizer (tdhF)	50.82	
M376 H9	H-P1453	conserved hypothetical protein	82.17	
M376 A10	H-P1454	hypothetical protein	33.44	
M376 B10	H-P1455	hypothetical protein	14.41	
M376 C10	H-P1456	membrane-associated lipoprotein (lpp20)	19.36	
M376 D10	H-P1457	hypothetical protein	23.21	
M376 E10	H-P1458	thioredoxin	11.55	
M376 F10	H-P1461	cytochrome c551 peroxidase	38.61	
M377 A1	H-P1462	secreted protein involved in flagellar motility	19.03	
M377 B1	H-P1463	hypothetical protein	24.86	
M377 C1	H-P1464	conserved hypothetical secreted protein	29.92	
M377 D1	H-P1465	ABC transporter, ATP-binding protein (H11087)	28.82	
M377 E1	H-P1466	conserved hypothetical integral membrane protein	41.58	
M377 F1	H-P1467	hypothetical protein	25.52	
M377 G1	H-P1468	branched-chain-amino-acid aminotransferase (ilvE)	37.51	
M377 H1	H-P1469	outer membrane protein (omp31)	27.39	
M377 A2	H-P1473	hypothetical protein	21.12	
M377 B2	H-P1474	thymidylate kinase (tmk)	21.12	
M377 C2	H-P1475	lipopolysaccharide core biosynthesis protein (kdtB)	17.38	
M377 D2	H-P1476	phenylacrylic acid decarboxylase	20.68	
M377 E2	H-P1479	hypothetical protein	92.95	
M377 F2	H-P1480	seryl-tRNA synthetase (serS)	45.76	
M377 G2	H-P1481	hypothetical protein	29.26	
M377 H2	H-P1482	hypothetical protein	9.57	
M377 A3	H-P1483	gerC2 protein (gerC2)	27.17	
M377 B3	H-P1484	conserved hypothetical integral membrane protein	16.39	
M377 C3	H-P1485	proline dipeptidase (pepQ)	21.01	
M377 D3	H-P1486	conserved hypothetical integral membrane protein	41.47	
M377 E3	H-P1487	conserved hypothetical integral membrane protein	40.26	

M377 F3	H-P1488	conserved hypothetical secreted protein	36.3	
M377 G3	H-P1489	lipase-like protein	56.21	
M381 G1	H-P1490	hemolysin	49.5	
M377 H3	H-P1491	phosphate permease	58.74	
M377 A4	H-P1492	conserved hypothetical nifU-like protein	9.9	
M377 B4	H-P1493	hypothetical protein	22.44	
M377 C4	H-P1494	UDP-MurNac-tripeptide synthetase (murE)	49.28	
M377 D4	H-P1495	transaldolase (tal)	34.87	
M377 E4	H-P1496	general stress protein (ctc)	19.69	
M377 F4	H-P1497	peptidyl-tRNA hydrolase (pth)	20.57	
M377 G4	H-P1499	hypothetical protein	30.03	
M377 H4	H-P1501	outer membrane protein (omp32)	42.79	
M377 A5	H-P1502	hypothetical protein	16.06	
M377 B5	H-P1503	cation-transporting ATPase, P-type (copA)	86.79	
M377 C5	H-P1504	conserved hypothetical protein	26.29	
M377 D5	H-P1505	riboflavin biosynthesis protein (ribG)	37.95	
M377 E5	H-P1506	glutamate permease (gltS)	44.99	
M377 F5	H-P1507	conserved hypothetical ATP-binding protein	42.46	
M381 F2	H-P1508	ferredoxin-like protein	50.49	
M377 G5	H-P1509	conserved hypothetical integral membrane protein	28.93	
M377 H5	H-P1510	conserved hypothetical protein	12.98	
M377 A6	H-P1511	hypothetical protein	11.99	
M377 B6	H-P1512	iron-regulated outer membrane protein (frpB)	96.58	
M377 C6	H-P1513	selenocystein synthase (selA)	42.57	
M377 D6	H-P1514	transcription termination factor NusA (nusA)	43.56	
M377 E6	H-P1518	hypothetical protein	10.56	
M381 B3	H-P1521	type III restriction enzyme R protein (res)	106.48	
M381 C3	H-P1523	DNA recombinase (recG)	68.64	
M377 F6	H-P1524	hypothetical protein	12.76	
M377 G6	H-P1525	hypothetical protein	23.32	
M377 H6	H-P1526	exodeoxyribonuclease (lexA)	27.61	
M377 A7	H-P1527	hypothetical protein	52.8	
M377 B7	H-P1530	purine nucleoside phosphorylase (punB)	19.91	
M377 C7	H-P1531	hypothetical protein	8.8	
M377 D7	H-P1532	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	65.78	
M377 E7	H-P1533	conserved hypothetical protein	25.52	
M377 F7	H-P1534	IS605 transposase (tnpB)	47.08	
M377 G7	H-P1535	IS605 transposase (tnpA)	15.73	
M377 H7	H-P1541	transcription-repair coupling factor (trcF)	110	

M377 A8	H-P1548	conserved hypothetical integral membrane protein	12.43	
M377 B8	H-P1551	conserved hypothetical secreted protein	14.08	
M377 C8	H-P1552	Na ⁺ /H ⁺ antiporter (nhaA)	48.29	
M381 B4	H-P1554	ribosomal protein S2 (rps2)	29.15	
M381 D4	H-P1555	translation elongation factor EF-Ts (tsf)	39.16	
M377 D8	H-P1556	cell division protein (ftsI)	67.76	
M381 E4	H-P1557	flagellar basal-body protein (fliE)	12.1	
M381 F4	H-P1558	flagellar basal-body rod protein (flgC) (proximal rod protein)	17.82	
M381 G4	H-P1559	flagellar basal-body rod protein (flgB) (proximal rod protein)	15.51	
M378 A1	H-P1560	cell division protein (ftsW)	42.79	
M378 B1	H-P1561	iron(III) ABC transporter, periplasmic iron-binding protein (ceuE)	36.96	
M378 C1	H-P1562	iron(III) ABC transporter, periplasmic iron-binding protein (ceuE)	36.74	
M378 D1	H-P1563	alkyl hydroperoxide reductase (tsaA)	21.89	
M378 E1	H-P1564	outer membrane protein	29.92	
M378 F1	H-P1565	penicillin-binding protein 2 (pbp2)	64.79	
M378 G1	H-P1566	hypothetical protein	16.28	
M378 H1	H-P1567	conserved hypothetical ATP-binding protein	22.99	
M378 A2	H-P1568	hypothetical protein	20.24	
M378 B2	H-P1569	hypothetical protein	21.78	
M378 C2	H-P1570	conserved hypothetical protein	18.15	
M378 D2	H-P1571	rare lipoprotein A (rlpA)	34.76	
M378 E2	H-P1572	regulatory protein DniR	41.03	
M378 F2	H-P1573	conserved hypothetical protein	28.05	
M378 G2	H-P1576	ABC transporter, ATP-binding protein (abc)	36.08	
M378 H2	H-P1577	ABC transporter, permease protein (yaeE)	23.76	
M378 A3	H-P1580	hypothetical protein	24.31	
M378 B3	H-P1581	methicillin resistance protein (llm)	37.07	
M378 C3	H-P1582	pyridoxal phosphate biosynthetic protein J (pdxJ)	28.93	
M378 D3	H-P1583	pyridoxal phosphate biosynthetic protein A (pdxA)	33.88	
M378 E3	H-P1584	sialoglycoprotease (gcp)	37.51	
M378 F3	H-P1585	flagellar basal-body rod protein (flgG)	28.93	
M378 G3	H-P1587	conserved hypothetical protein	17.16	
M378 H3	H-P1588	conserved hypothetical protein	27.94	
M381 H1	H-P1590	hypothetical protein	4.4	

M318 G2	H-S38729	autoimmune antigen Ku, p70 subunit	67.1	67
H1	H-S39329	Kallikrein I (renal/pancreas/salivary) {alternative products}	24.64	30
M270 G4	H-S43855	Recoverin, photoreceptor protein	22.11	32.0kDa
M300 C2	H-S56151	milk fat globule protein HMFG	24.09	30
M318 C1	H-S57153	retinoblastoma-binding protein 1, isoform I [RBBP1]	101.31	101
M271 B2	H-S57162	retinoblastoma-binding protein 1, isoform III [RBBP1], INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE RETINOBLASTOMA PROTEIN.	93.72	110
M317 H3	H-S62027	transducin, gamma subunit	8.25	11
M270 G6	H-S66793	arrestin, X-arrestin=S-antigen homolog [human, retina, mRNA, 1314 nt], MAY PLAY A ROLE IN AN AS YET UNDEFINED RETINA-SPECIFIC SIGNAL TRANSDUCTION.	42.79	50.0kDa
M419 C2	H-S67859	"transcription initiation factor IIe, alpha subunit"	48.360	64.0kDa
M302 D7	H-S69022	myosin, light polypeptide 2, ventricular	18.26	31
H5	H-S69272	cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt]	41.47	50
D1	H-S72043	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]	7.59	19
M266 B3	H-S74221	cytokine IK factor	17.93	36.0kDa
D1	H-S74445	cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]	15.18	23
E3	H-S74728	antiquitin=26g turgor protein homolog [human, kidney, mRNA, 1809 nt]	56.32	53
D4	H-S75174	E2F transcription factor 4, p107/p130-binding	45.87	58
166-61	H-S76474	"trkB {alternately spliced} [human, brain, mRNA]"	55	52.54
169-40	H-S76617	"B1k=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]"	60	55.62
M250 D3	H-S79522	ubiquitin carboxyl-terminal extension protein, Ubiquitin A-52 residue ribosomal protein fusion product 1	17.27	17.0kDa
M236 B4	H-S80562	calponin, acidic	36.3	49

G1	H-S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	37.73	34
M313 E1	H-S85655	prohibitin [PHB]	30.03	40.0kDa
M465 A6	H-S87759	protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]	42.13	52.0kDa
M472 B1	H-U00803	tyrosine-protein kinase FRK	55.620	64.0kDa
B2	H-U02390	Human adenylyl cyclase-associated protein homolog CAP2 (CAP2) mRNA, complete cds	52.58	55
167-2	H-U02680	human protein tyrosine kinase mRNA	36	38.57
G2	H-U03056	Human tumor suppressor (LUCA-1) mRNA, complete cds	47.96	47
M512 E3	H-U03100	Human alpha2(E)-catenin mRNA, complete cds	102.52	102.0kDa
M306 G3	H-U03187		72.93	95.0kDa
H3	H-U03398	Human receptor 4-1BB ligand mRNA, complete cds	28.05	51
D3	H-U03486	Human connexin40 gene, complete cds	39.49	40
M300 C3	H-U03643	leukophysin	25.96	34
F5	H-U03749	Human chromogranin A (CHGA) gene, promoter and	50.38	50
M314 C3	H-U03886	GS2 (GB:U03886)	27.94	32.0kDa
M306 E3	H-U04343	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) [CD86]	35.64	47
167-61	H-U05012	TrkC	92	90.82
M302 G5	H-U05340	cell division cycle protein p55	55	55
A4	H-U05659	Hydroxysteroid (17-beta) dehydrogenase 3	34.21	36
F1	H-U05861	Human hepatic dihydrodiol dehydrogenase gene	35.64	40
M302 B2	H-U06452	antigen MART-1, melanoma	13.09	20.0kDa
169-52	H-U06454	human AMP-activated protein kinase (hAMPK) mRNA	70	60.79
M315 A3	H-U06643	lectin, epidermal	15.07	18
H1	H-U06715	Cytochrome B561	27.06	25
M476 E5	H-U07132	Human steroid hormone receptor Ner-I mRNA, complete cds	50.82	55.0kDa
M236 D3	H-U07151	guanine nucleotide-binding protein ADP-ribosylation factor like gene 3	20.13	34
M317 G3	H-U07559	homeotic protein Islet-1	38.17	38
M266 H1	H-U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds	40.37	40
E3	H-U07919	Aldehyde dehydrogenase 6	56.43	53

M298 A3	H-U08021	nicotinamide N-methyltransferase	29.15	36.0kDa
M297 B1	H-U08024	alcohol/hydroxysteroid sulfotransferase	31.46	50.0kDa
A2	H-U08336	Human basic helix-loop-helix transcription factor mRNA, complete cds	21.89	42
E2	H-U09303	Human T cell leukemia LERK-2 (EPLG2) mRNA, complete cds	38.17	40
M250 H5	H-U09559	RCH1, RAG (recombination activating gene) cohort 1	58.3	58.0kDa
167-50	H-U09564	human serine kinase mRNA	72	72.12
166-74	H-U09578	human MAPKAP kinase (3pK) mRNA	50	42.09
M302 C4	H-U09813	ATP synthase, subunit 9, mitochondrial	15.73	30
A1	H-U09850	Zinc finger protein 143 (clone pHZ-1)	68.97	68
M423 E1	H-U09937	Human urokinase-type plasminogen receptor	36.96	49.0kDa
M450 H4	H-U10117	Human endothelial-monocyte activating polypeptide II mRNA, complete cds	34.43	38.0kDa
M314 G1	H-U10248	ribosomal protein L29	17.6	27
M298 H1	H-U10323	nuclear factor 45	44.77	45
E1	H-U10492	Human Mox1 protein (MOX1) mRNA, complete cds	28.05	37
F3	H-U10686	Human MAGE-11 antigen (MAGE11) gene, complete cds	35.2	35
167-38	H-U11050	human NIMA-like protein kinase 1 (NLK1) mRNA	55	49.02
M266 B2	H-U11292	Human Ki nuclear autoantigen mRNA, complete cds, may play a rol in cell adhesion	29.48	32
167-62	H-U11791	human cyclin H m RNA	40	35.60
M423 D5	H-U12255	immunoglobulin gamma heavy chain Fc receptor RI, high affinity	40.26	48.0kDa
M302 F7	H-U12404	Csa-19	23.98	32
M236 A2	H-U12465	ribosomal protein L35	13.64	24
169-4	H-U12535	human epidermal growth factor receptor kinase substrate (Eps8) mRNA	100	90.49
F3	H-U12597	Human tumor necrosis factor type 2 receptor associated protein (TRAP3) mRNA, complete cds	55.22	64
M314 D1	H-U12979	transcriptional coactivator PC4	14.08	23
M476 G4	H-U13044	GA-binding protein transcription factor, alpha subunit (60kD)	50.05	53.0kDa
M302 F3	H-U13665	cathepsin O (GB:U13665)	36.3	50.0kDa
M311 G4	H-U13831	cellular retinol binding protein II	14.85	20.0kDa
A2	H-U13991	Human TATA-binding protein associated factor 30 kDa subunit (tafII30) mRNA, complete cds	24.09	34

M416 A4	H-U14187	Human receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA, complete cds	26.29	29.0kDa
M250 A2	H-U14188	eph-related receptor tyrosine kinase ligand 4 [EPLG4]	22.22	27
M302 D2	H-U14193	human TFIIA gamma subunit mRNA	12.060	28.0kDa
M416 G1	H-U14603	Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence	18.48	30.0kDa
E2	H-U14747	Visinin-like 1	21.12	25
M266 D4	H-U14966	ribosomal protein L5	32.78	38
M314 E2	H-U14967	ribosomal protein L21	17.71	29
M266 F5	H-U14968	ribosomal protein L27a	16.39	19.0kDa
M248 E3	H-U14969	ribosomal protein L28	15.18	27
M266 E1	H-U14971	ribosomal protein S9	21.45	30
M250 C2	H-U15009	small nuclear ribonucleoprotein, Sm D3	13.97	17.0kDa
M311 D4	H-U16660	enoyl-Coenzyme A hydratase-like protein, peroxisomal	36.19	38
M302 H4	H-U17074	cyclin-dependent kinase 6 inhibitor p18	18.59	29
M306 A2	H-U17195	A-kinase anchor protein 100 [AKAP100*]	72.05	100
D1	H-U17280	Steroidogenic acute regulatory protein	31.46	35
M316 F1	H-U18291	cell division cycle protein 16	68.2	71.0kDa
C5	H-U18420	Human ras-related small GTP binding protein Rab5 (rab5) mRNA, complete cds	23.87	33
M311 A2	H-U18423	spinal muscular atrophy gene	32.45	41
M248 D4	H-U18914	hypothetical protein, (Human 19.8 kDa protein mRNA, complete cds)	20.35	32
M302 B5	H-U19718	microfibril-associated glycoprotein 2	20.24	34.0kDa
M305 E3	H-U20240	CCAAT/enhancer-binding protein gamma	16.61	29
M302 A8	H-U20352	malate dehydrogenase	36.85	40
M416 F4	H-U20391	Human folate receptor (FOLR1) gene, complete cds	28.38	34.0kDa
M311 D1	H-U20536	apoptotic cysteine protease Mch2	32.34	38.0kDa
M431 G2	H-U20659	RNA polymerase II, subunit B7	19.03	31.0kDa
M499 C1	H-U20938	Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete cds	112.86	100.0kDa
M305 F2	H-U20972	14-3-3 protein, epsilon	28.16	36
M271 D3	H-U21049	hypothetical protein (GB:U21049), ESTs, Highly similar to DD96 [H.sapiens].	12.65	16
M421 G5	H-U21858	Human transcriptional activation factor TAFII32 mRNA, complete cds	29.15	38.0kDa

M424 H3	H-U22662	Human nuclear orphan receptor LXR-alpha mRNA, complete cds	49.28	49.0kDa
M271 D2	H-U24074	killer cell inhibitory receptor [KIR], Homo sapiens natural killer-associated transcript 3 (NKAT3), complete cds. RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.	37.62	43
169-29	H-U24153	human p21-activated protein kinase (Pak2) gene	60	57.82
M385 H2	H-U24166	EBI	29.59	36.0kDa
G1	H-U24169	Human JTV-1 (JTV-1) mRNA, complete cds	34.43	40
E1	H-U24576	Human breast tumor autoantigen mRNA, complete sequence	18.26	27
G4	H-U24577	Human LDL-phospholipase A2 mRNA, complete cds	48.62	52
H1	H-U25789	Human ribosomal protein L21 mRNA, complete cds	17.71	32
M416 D1	H-U25849	Human red cell-type low molecular weight acid phosphatase (ACP1) gene, 5' flanking region and	17.49	28.0kDa
M300 A3	H-U26312	heterochromatin protein H-PIHs-gamma	19.14	30
M416 D3	H-U26403	Human receptor tyrosine kinase ligand LERK-7 precursor (EPLG7) mRNA, complete cds	25.19	30.0kDa
M317 E2	H-U27143	human protein kinase C inhibitor-I cDNA	13.900	17.0kDa
E5	H-U28249	Human 11kd protein mRNA, complete cds	12.32	12
F4	H-U28386	Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds	58.3	54
M423 E3	H-U28694	Chemokine (C-C) receptor 3	39.16	39.0kDa
M266 G6	H-U28963	Gps2	36.08	36
M306 D3	H-U30610	CD94 antigen (NK/T-cell C-type lectin receptor) [CD94]	19.8	27
B1	H-U31116	Human beta-sarcoglycan A3b mRNA, complete cds	35.09	33
M297 C2	H-U31278	mitotic feedback control protein Madp2 homolog	22.66	31.0kDa
M302 G2	H-U31384	guanine nucleotide-binding protein, gamma 11 subunit	8.14	10
F4	H-U31986	Human cartilage-specific homeodomain protein Cart-1 mRNA, complete cds	35.97	47
M390 F3	H-U32114	caveolin 2	17.93	18.0kDa
E4	H-U32324	Human interleukin-11 receptor alpha chain mRNA, complete cds	46.53	54
F1	H-U32576	Apolipoprotein C-IV	14.08	16
M298 C4	H-U32907	p37NB protein	34.54	39

M300 D3	H-U32944	dynein, light chain 1, cytoplasmic	9.9	15
M297 D1	H-U32989	tryptophan 2,3-dioxygenase	44.77	50.0kDa
166-51	H-U33052	"protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA]"	110	108.3
166-64	H-U33054	"human G protein-coupled receptor kinase GRK4 mRNA, alpha splice variant"	52	63.65
166-88	H-U33055	"human G protein-coupled receptor kinase GRK4 mRNA, beta splice variant"	60	60.1
166-76	H-U33056	"human G protein-coupled receptor kinase GRK4 mRNA, gamma splice variant"	58	58.59
A2	H-U34584		17.71	31
169-87	H-U34820	human MAP kinase mRNA	55	46.49
215-2	H-U34822	human JNK1 alpha2 protein kinase (JNK1A2) mRNA	55	47.04
169-37	H-U35002	human JNK2 beta1 protein kinase (JNK2B1) mRNA	50	42.09
169-25	H-U35003	human JNK2 beta2 protein kinase (JNK2B2) mRNA	55	46.71
167-16	H-U35004	human JNK1 beta1 protein kinase (JNK1B1) mRNA	52	42.31
M300 B2	H-U35048	TSC-22 protein	15.95	27
M423 E5	H-U35398	Human G protein-coupled receptor mRNA, complete cds	40.26	48.0kDa
A3	H-U35735	Human RACH1 (RACH1) mRNA, complete cds	42.9	78
M250 E5	H-U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit, transforming growth factor-beta receptor II interacting protein 1	35.86	36.0kDa
M270 E4	H-U37283	microfibril-associated glycoprotein-2 (GB:U37283)	19.14	32
M426 F3	H-U37352	Protein phosphatase 2A, regulatory subunit B' alpha-1	56.65	55.0kDa
E1	H-U37529	Human substance P beta-PPT-A mRNA, complete cds	14.3	22
M305 H5	H-U37547	apoptosis inhibitor	68.09	64
M424 D5	H-U38480	Human retinoid X receptor-gamma mRNA, complete cds	51.04	61.0kDa
M270 F4	H-U38810	Human mab-21 cell fate-determining protein homolog (CAGR1) mRNA,		
M467 F6	H-U38904	Human zinc finger protein C2H2-25 mRNA, complete cds	40.48	47.0kDa
E2	H-U39318	Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds	16.28	22
166-75	H-U39657	human MAP kinase kinase 6 (MKK6) mRNA	40	36.81
M298 E4	H-U39945	human adenylate kinase 2 (adk2) mRNA	26.3633	38.0kDa

166-38	H-U40282	human integrin-linked kinase (ILK) mRNA	55	49.68
169-65	H-U40343	human CDK inhibitor p19INK4d mRNA	18	18.33
E2	H-U40705	Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds	48.4	52
166-50	H-U40989	human tat interactive protein mRNA	60	53.09
M266 H6	H-U41767	metargidin precursor	89.65	90
M270 F3	H-U41804	Human putative T1/ST2 receptor binding protein precursor mRNA, complete cds	25.08	35.0kDa
D5	H-U42360	Human N33 gene	38.28	38
A1	H-U43368	Vascular endothelial growth factor B	22.88	33
M421 G7	H-U43901	Human 37 kD laminin receptor precursor/p40 ribosome associated protein gene, complete cds	32.56	58.0kDa
M392 C2	H-U43923	transcription factor SUPTH4	12.98	16.0kDa
E2	H-U46024	Myotubular myopathy 1	66.44	58
M330 A1	H-U46838	p105MCM	90.42	97
M476 E2	H-U47677	Human transcription factor E2F1 (E2F1) gene, promoter and	48.18	53.0kDa
M421 H1	H-U48707	Human protein phosphatase-1 inhibitor mRNA, complete cds	18.92	36.0kDa
M302 B7	H-U49070	peptidyl-prolyl isomerase PIN1	18.04	28.0kDa
C1	H-U49188	Human placenta (Diff33) mRNA, complete cds	54.45	70
M485 H2	H-U49837	Human LIM protein MLP mRNA, complete cds	21.45	34.0kDa
D2	H-U49897	Homo sapiens phenylalanine hydroxylase (PAH) mRNA, complete cds	49.83	64
B2	H-U49957	Human LIM protein (LPP) mRNA, partial cds	67.43	67
166-16	H-U50196	human adenosine kinase mRNA	50	38.02
A4	H-U50939	Human amyloid precursor protein-binding protein 1 mRNA, complete cds	58.85	60
G3	H-U51224	Human U2AFBPL gene, complete cds	52.8	55
M486 E3	H-U51333	Hexokinase 3 (white cell)	101.64	100.0kDa
M305 D1	H-U51478	ATPase, Na ⁺ /K ⁺ transporting, beta 3 subunit	30.8	36

M416 H3	H-U52112	Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene	25.96	36.0kDa
M463 E1	H-U53442	human p38Beta MAP kinase mRNA	40.99	49.0kDa
G3	H-U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds	84.81	98
M463 C1	H-U54617	human pyruvate dehydrogenase kinase isoform 4 mRNA	45.28	52.0kDa
169-38	H-U54645	methylmalonyl-coA mutase precursor	38	25.59
M300 H3	H-U56255	t-complex sterility protein homolog CW-1	12.54	16
C4	H-U56417	Human lysophosphatidic acid acyltransferase-alpha mRNA, complete cds	31.24	46
M305 A2	H-U56637	actin-capping protein alpha subunit isoform 1	31.57	31
M235 E6	H-U56814	Human DNaseI-Like III protein (DNASIL3) mRNA, complete cds, involved in apoptosis Binds specifically to G-ACTIN AND BLOCKS ACTIN POLYMERIZATION.	33.66	40.0kDa
D5	H-U57059		31.02	36
B3	H-U57093	Human small GTP-binding protein rab27b mRNA, complete cds	24.09	34
D3	H-U57099	Human APEG-1 mRNA, complete cds	12.54	20
F1	H-U58331	Sarcoglycan, delta (35kD dystrophin-associated glycoprotein)	28.27	24
M512 F4	H-U58334	Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds	110.66	108.0kDa
B3	H-U58516	Human breast epithelial antigen BA46 mRNA, complete cds	42.68	50
M250 E4	H-U58522	Human huntingtin interacting protein (HIP2) mRNA, complete cds	22.11	30

M419 G2	H-U60207	human stress responsive serine/threonine protein kinase Krs-2 mRNA	53.640	63.0kDa
M298 B2	H-U60276	arsA homolog (hASNA-I)	36.63	47.0kDa
B2	H-U60521	Human protease proMch6 (Mch6) mRNA, complete cds	45.87	52
F3	H-U61166	Human SH3 domain-containing protein SH3P17 mRNA, complete cds	57.31	57
M250 B5	H-U61232	cofactor E (tubulin-folding protein), REQUIRED FOR VIABILITY IN THE ABSENCE OF THE KINESIN-RELATED CIN8		
A5	H-U62392	Homo sapiens zinc finger protein mRNA, complete cds	43.45	52
G1	H-U62801	Human protease M mRNA, complete cds	26.95	33
M266 B1	H-U62962	Int-6 , Human Int-6 mRNA, complete cds	49.06	52.0kDa
M300 G1	H-U63295	seven in absentia homolog	31.13	36
M306 H3	H-U64198		94.93	98
H3	H-U64863	Human hPD-1 (hPD-1) mRNA, complete cds	31.79	37
B3	H-U65581	Human ribosomal protein L3-like mRNA, complete cds	44.88	52
M341 D1	H-U65918	DAZ homologue [DAZLA]	32.56	36.0kDa
M302 E1	H-U65928	Jun activation domain binding protein	36.85	48.0kDa
M512 D3	H-U66347	Homo sapiens cAMP phosphodiesterase (PDE4C) mRNA, 4C-426 isoform, complete cds	46.97	60.0kDa
M306 F3	H-U66867	ubiquitin-conjugating enzyme E2I [UBE2I]	17.49	28
M416 E2	H-U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene	22.66	37.0kDa
F2	H-U68382	Mannosidase, alpha B, lysosomal	35.64	36
G2	H-U69141	Glutaryl-Coenzyme A dehydrogenase	48.29	56
B2	H-U70660	Human copper transport protein HAH1 (HAH1) mRNA, complete cds	7.59	16
M297 B2	H-U71374	peroxisomal membrane protein (Pex13p)	40.15	40.0kDa
M306 A3	H-U75272	progastricin [PGC]	42.79	49.0kDa
A2	H-U75285	Homo sapiens apoptosis inhibitor survivin gene, complete cds	15.73	25
B2	H-U77456	Human nucleosome assembly protein 2 mRNA, complete cds	41.36	50
C2	H-U78294	Homo sapiens 15S-lipoxygenase mRNA, complete cds	74.47	74
F6	H-U78302	Human 2,4-dienoyl-CoA reductase gene	36.96	40

M478 G3	H-U78798	Human TNF receptor associated factor 6 (TRAF6) mRNA, complete cds	57.53	65.0kDa
G3	H-U80982	Human myeloid-specific C/EBP-epsilon transcription factor (CEBPE) gene, complete cds	27.5	51
M468 B7	H-U82256	Homo sapiens arginase type II mRNA, complete cds	39.05	45.0kDa
M465 B2	H-U82812	Human scavenger receptor cysteine rich Sp alpha mRNA, complete cds	38.28	48.0kDa
M484 D7	H-U83410	Human CUL-2 (cul-2) mRNA, complete cds	82.06	85.0kDa
M467 E6	H-U83460	Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds	21.01	32.0kDa
D2	H-U84763	Homo sapiens UCP3 mRNA, complete cds	34.43	42
B2	H-U86070	Homo sapiens phosphomannomutase mRNA, complete cds	28.93	36
C2	H-U90441	Human prollyl 4-hydroxylase alpha (II) subunit mRNA, complete cds	58.96	64
B2	H-U90543	Human butyrophilin (BTF1) mRNA, complete cds	58.08	54
H2	H-U90545	Human sodium phosphate transporter (NPT4) mRNA, complete cds	44.22	36
G2	H-U90552	Human butyrophilin (BTF5) mRNA, complete cds	56.54	48
C3	H-U91521	Peroxisomal biogenesis factor 12	39.6	48
H1	H-U91641	Human alpha2,8-sialyltransferase mRNA, complete cds	41.47	45
C1	H-U93869	Human RNA polymerase III subunit (RPC39) mRNA, complete cds	34.98	36
F2	H-U94346	Human calpain-like protease (htra-3) mRNA, complete cds	70.4	65
C2	H-U94855	Human translation initiation factor 3 47 kDa subunit mRNA, complete cds	39.38	36
M271 F7	H-U95089	Epidermal growth factor receptor.	44.66	47
M424 A5	H-U95847	Human GDNF receptor alpha mRNA, complete cds	50.71	52.0kDa
D2	H-U96094	Human sarcophilin (SLN) mRNA, complete cds	3.52	10
B3	H-U96769	Homo sapiens chondroadherin gene, 5'flanking region and	39.6	43
M298 G2	H-V00566	prolactin	25.08	35
M298 H2	H-V00571	corticotropin-releasing factor	21.67	49
217-61	H-V00572	phosphoglycerate kinase I	50	45.94
M314 B3	H-V00597	parathyroid hormone	12.76	14

M305 B8	H-X00129	retinol-binding protein 4, interstitial [RBP4]	22	51
F2	H-X00351	Human mRNA for beta-actin	41.36	41
A4	H-X00570	apolipoprotein C-I	9.24	35
M362 E1	H-X01057	interleukin 2 receptor, alpha [IL2RA]	30.03	40.0kDa
A4	H-X01677P	Human liver mRNA for glyceraldehyde-3-phosphate dehydrogenase (G3PD, EC 1.2.1.12)	10.45	10
M271 D6	H-X02152	lactate dehydrogenase A [LDHA], L-LACTATE DEHYDROGENASE M CHAIN	36.63	45.0kDa
A1	H-X02158	Human gene for erythropoietin	21.34	32
H4	H-X02415	Human gene for fibrinogen gamma chain	48.18	50
A5	H-X02750	Protein C (inactivator of coagulation factors Va and VIIIa)	50.82	53
M302 B3	H-X02751	proto-oncogene N-ras	20.9	25.0kDa
D3	H-X02812	Human mRNA for transforming growth factor-beta (TGF-beta)	43.12	50
M302 C1	H-X03124	tissue inhibitor of metalloproteinase 1	22.88	36.0kDa
M362 B1	H-X03342	ribosomal protein L32	14.96	24.0kDa
M235 A2	H-X03484	human mRNA for raf oncogene	71.350	73.0kDa
M318 A3	H-X03557	interferon-induced protein 56	52.69	50.0kDa
A3	H-X03747	ATPase, Na+/K+ transporting, beta 1 polypeptide	33.44	45
M305 D2	H-X04297	ATPase, Na+/K+ transporting, alpha subunit	112.64	99
M305 A5	H-X04327	2,3-bisphosphoglycerate mutase	28.6	36
M271 G5	H-X04588	tropomyosin TM30nm, cytoskeletal	26.29	40.0kDa
M305 C8	H-X04741	ubiquitin related protein	23.43	28.0kDa
M236 A5	H-X05231	matrix metalloproteinase 1 (interstitial collagenase) [MMP1], CLEAVES COLLAGENS	51.7	53.0kDa
166-53	H-X05246	"phosphoglycerate kinase, testis specific"	50	45.94
M236 A1	H-X05908	annexin I, REGULATES PHOSPHOLIPASE A2 ACTIVITY, Binds CALCIUM IONS	38.17	40
M250 A4	H-X06234	S100 calcium-binding protein A8 (calgranulin A)	10.34	10.0kDa
M266 B6	H-X06323	ribosomal protein L3, isoform 1	38.39	39
M313 A7	H-X06617	ribosomal protein S11	17.49	27
M416 E4	H-X06948	High affinity IgE receptor alpha-subunit (FcERI)	28.38	36.0kDa
M421 H7	H-X07203	Human mRNA for CD20 receptor (S7)	32.78	40.0kDa
217-2	H-X07743	pleckstrin	38	38.57

217-73	H-X07767	"cAMP-dependent protein kinase, alpha-catalytic subunit"	45	38.68
M305 B3	H-X07898	troponin C, skeletal, fast	17.71	25
M306 E1	H-X07979	integrin, beta 1	87.89	110
A11	H-X08004	ras-related protein rap1B	20.24	38
M235 A7	H-X12387	Cytochrome P450 IIIA3 (nifedipine oxidase chain 3)	55.44	60.0kDa
M315 F1	H-X12496	glycophorin C	14.19	24
M316 D3	H-X12517	small nuclear ribonucleoprotein U1, C	17.6	30.0kDa
M236 E5	H-X12534	guanine nucleotide-binding protein rap2, ras-oncogene related	20.24	34.0kDa
M266 E3	H-X12597	High-mobility group (nonhistone chromosomal) protein 1, placenta	23.76	37
217-14	H-X12656	human mRNA for protein phosphatase 2A (beta type)	40	34.06
H4	H-X12662	H.sapiens arginase gene exon 1 and flanking regions (EC 3.5.3.1) (and joined CDS)	35.53	50
C1	H-X12953	RAB2, member RAS oncogene family	23.43	29
F5	H-X13956	Human 12S RNA induced by poly(rI), poly(rC) and Newcastle disease virus	9.13	19
M297 A1	H-X15005	laminin receptor 1	33.11	48.0kDa
M315 E3	H-X15088	guanine nucleotide binding protein (G protein), alpha transducing (transducin) activity polypeptide 1 [GNAT1]	38.61	45
G2	H-X15183	Human mRNA for 90-kDa heat-shock protein	80.63	80
M385 C1	H-X15422	mannose-binding lectin, soluble (opsonic defect) [MBL]	27.39	27.0kDa
M271 D7	H-X15606	INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR [Homo sapiens].	30.36	37.0kDa
M298 C5	H-X15653	uracil-DNA glycosylase	33.55	37
M302 B4	H-X15822	cytochrome-c oxidase, VIIa subunit, liver	9.24	20
M305 A6	H-X15940	ribosomal protein L31	13.86	18
M236 G5	H-X15949	interferon regulatory factor 2 , BINDS AND REPRESSES REGULATORY REGION OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES.	38.5	54.0kDa
M236 C2	H-X16064	translationally-controlled tumor protein	19.03	35
M512 B5	H-X16323	Hepatocyte growth factor (hepapoietin A)	80.19	100.0kDa
M315 C3	H-X16461	cell division cycle 2, G1 to S and G2 to M [CDC2]	32.78	40
M297 G2	H-X16832	cathepsin H	36.96	45.0kDa

M271 B1	H-X16983	integrin, alpha 4 (CD49D, alpha 4 subunit of VLA-4 receptor) [ITGA4], IMPORTANT FOR CELL-CELL ADHESION FUNCTION.	114.29	114
M270 A7	H-X17025	plasminogen activator-inducible c54, Human homolog of yeast IPP isomerase	25.19	34
M302 C3	H-X17042	proteoglycan 1, secretory granule	17.49	26
B1	H-X17206	ribosomal protein S2	24.42	45
B4	H-X17254	Transcription factor Eryf1	45.54	53
M311 H2	H-X17610	beta-1-glycoprotein, pregnancy-specific (GB:X17610)	46.97	48.0kDa
M315 D1	H-X17644	G1 to S phase transition protein (GST1)	55	55
M340 G1	H-X51415	lipase, hormone-sensitive [LIPE]	84.59	98.0kDa
M464 A7	H-X51688	Cyclin A	47.63	47.0kDa
M313 G1	H-X51745	major histocompatibility complex, class I, A	40.26	50
M297 A2	H-X51804	putative receptor protein PMI	21.23	30
D4	H-X51952	Human UCP gene for uncoupling protein exons 1 and 2	33.88	37
M300 B1	H-X52011	muscle determining factor	26.73	39
M419 G1	H-X52479	"protein kinase c, alpha type"	82.28	85.0kDa
A2	H-X52486	Uracil-DNA glycosylase	35.97	36
E3	H-X52520	Tyrosine aminotransferase	50.05	58
B1	H-X52638	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	51.92	47
M509 C4	H-X52730	Human gene for phenylethanolamine N-methylase (PNMT) (EC 2.1.1.28)	31.13	35.0kDa
M235 C5	H-X52839	ribosomal protein L17	15.51	18
M426 C2	H-X52943	Human mRNA for ATF-a transcription factor	53.24	64.0kDa
M266 G5	H-X53777	ribosomal protein L23	20.35	31
B4	H-X53961	Lactotransferrin	78.32	78
M462 C6	H-X54150	Fc fragment of IgA, receptor for	31.68	37.0kDa
M302 A6	H-X54304	myosin, light polypeptide 2, regulatory	18.92	32.0kDa
M311 G2	H-X54802	cytochrome-c oxidase, IV subunit	18.7	23.0kDa
M270 H3	H-X54871	guanine nucleotide-binding protein Rab5B, ras-oncogene related [RAB5B], PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR TRAFFIC (BYSIMILARITY).	23.76	33.0kDa
M313 B6	H-X54936	placenta growth factor [PLGF*]	16.5	22.0kDa
M496 B2	H-X55079	Human lysosomal alpha-glucosidase gene exon 1	104.83	98.0kDa
D1	H-X55330	Aspartylglucosaminidase	38.17	36

E1	H-X55448	H.sapiens G6PD gene for glucose-6-phosphate dehydrogenase	25.41	30
M421 G6	H-X56253	Human MPR46 gene for 46kd mannose 6-phosphate receptor	30.58	52.0kDa
169-89	H-X56468	14-3-3 protein tau	34	27.02
M300 B4	H-X56549	fatty-acid-binding protein, muscle	14.74	17
M298 D2	H-X56740	guanine nucleotide-binding protein rab11 [RAB11*]	23.87	31.0kDa
M266 E5	H-X56932	highly basic protein, 23 kDa	22.44	30.0kDa
M318 G1	H-X57025	insulin-like growth factor I	16.94	18
M305 F5	H-X57348	protein kinase C inhibitor	27.39	35.0kDa
M236 D6	H-X57351	interferon-induced protein 1-8D	14.63	24
H3	H-X57352	interferon-induced protein 1-8U	14.74	38
M305 B6	H-X58079	S-100 protein, alpha chain	10.45	11
E6	H-X59131	H.sapiens D13S106 mRNA for a highly charged amino acid sequene	34.76	50
M248 H5	H-X59268	transcription factor IIB [TCF2B*]	34.87	49
E2	H-X59357	Epstein-Barr virus small RNA-associated protein	14.19	36
M236 D4	H-X59417	macropain, iota subunit , THE INTERACTION OF CALPONIN WITH ACTIN INHIBITS ACTOMYOSIN MG-ATPASE ACTIVITY	27.17	36
M271 H4	H-X59618	ribonucleotide reductase, small subunit	42.9	46
M250 G3	H-X59710	CAAT-box DNA-binding protein, subunit B, CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A [Homo sapiens]	22.66	34
M423 E2	H-X59711	Nuclear transcription factor Y, alpha	38.28	48.0kDa
M271 C7	H-X59798	Cyclin D1 (PRAD1; parathyroid adenomatosis 1). ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION.	32.56	40.0kDa
M270 H5	H-X59834	calmodulin	41.14	53.0kDa
M416 D5	H-X59871	Transcription factor 7 (T-cell specific)	29.59	36.0kDa
M485 D6	H-X60036	Phosphate carrier, mitochondrial	39.82	37.0kDa
M250 D4	H-X60489	translation elongation factor 1, beta	24.86	33.0kDa
F5	H-X60592	Human CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte activation molecule	30.58	46
M312 F3	H-X61587	ras-related rhoG	21.12	21.0kDa
F9	H-X61622	cyclin-dependent kinase 2 [CDK2]	32.89	56
M313 E3	H-X61970	macropain, zeta subunit	26.62	35.0kDa
M428 D1	H-X62055	tyrosine phosphatase, non-receptor type 6	65.78	66.0kDa

M248 C4	H-X62534	high mobility group protein 2, BINDS PREFERENTIALLY SINGLE-STRANDED DNA AND UNWINDS DOUBLE STRANDED DNA.	23.1	37
M305 F3	H-X62753	folate-binding protein	28.38	36
M476 G2	H-X63468	H.sapiens mRNA for transcription factor TFIIIE alpha	48.4	53.0kDa
G6	H-X63469	General transcription factor TFIIIE beta subunit, 34 kD	32.12	56
G4	H-X63522	H.sapiens mRNA DAUDI6 for retinoic acid X receptor b	58.74	54
M316 G2	H-X63526	translation elongation factor 1, gamma	48.18	52.0kDa
M305 C5	H-X63527	ribosomal protein L19	21.67	33
E2	H-X63629	Cadherin 3 (P-cadherin)	91.3	110
D4	H-X64037-2	General transcription factor IIF, polypeptide 1 (74kD subunit)	56.98	64
M302 C6	H-X64559	tetranectin	22.33	32.0kDa
M271 H1	H-X64728	choroideremia-like [CHML], H.sapiens CHML mRNA	72.27	98
M270 E1	H-X64810	proprotein convertase subtilisin/kexin type 1 [PCSK1], INVOLVED IN PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS	82.94	90
M311 F4	H-X64877	complement factor H-related protein	29.81	36.0kDa
M388 D1	H-X65293	protein kinase C, epsilon [PRKCE]	81.18	96.0kDa
B5	H-X65873	kinesin, heavy polypeptide	106.04	34
F4	H-X66079	Spi-B transcription factor (Spi-1/PU.1 related)	28.93	54
F3	H-X66114	2-oxoglutarate carrier protein [OGMT*]	0	37
M305 C6	H-X66141	myosin, light polypeptide 2, regulatory, ventricular	18.37	31
M419 H1	H-X66357	cell division protein kinase 3	33.620	44.0kDa
166-13	H-X66358	serine/threonine-protein kinase KKIALRE	45	39.45
166-25	H-X66360	serine/threonine-protein kinase PCTAIRE-2	60	57.60
M419 A2	H-X66363	serine/threonine-protein kinase PCTAIRE-1	54.600	64.0kDa
166-37	H-X66364	H.sapiens mRNA PSSALRE for serine/threonine protein kinase	38	32.19
M419 B2	H-X66365	cell division protein kinase 6	35.900	46.0kDa
H3	H-X66839	H.sapiens MaTu MN mRNA for p54/58N protein	50.6	54
M266 G3	H-X67325	interferon, alpha-inducible gene p27	13.53	13
M462 H7	H-X67594	Melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	34.98	44.0kDa

M236 C5	H-X67951	Proliferation-associated gene A (natural killer-enhancing factor A), PAGA	22	34
H3	H-X68486	Adenosine receptor A2	45.43	45
M429 E3	H-X68561	Sp4 transcription factor	86.35	86.0kDa
M430 F2	H-X69151	ATP synthase, H+ transporting, subunit C, vacuolar	42.13	58.0kDa
M236 C3	H-X69392	ribosomal protein L26	16.06	29
B3	H-X69532	H.sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 1-3	100.32	98
M236 F5	H-X69654	ribosomal protein S26	12.76	18
M421 C8	H-X70218	Protein phosphatase 4 (formerly X), catalytic subunit	33.88	
M266 H5	H-X70848	protein phosphatase 1, alpha catalytic subunit	36.41	37
E1	H-X70940	Eukaryotic translation elongation factor 1 alpha 2	51.04	60
M270 F1	H-X72215	[PIT1], POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)	32.12	40.0kDa
M271 A7	H-X72760	Laminin, beta 2 (laminin S), S-LAMININ IS A LAMININ-LIKE ADHESIVE PROTEIN CONCENTRATED IN THE SYNAPTIC CLEFT OF THE NEUROMUSCULAR JUNCTION.	67.87	75.0kDa
M235 B1	H-X72841	Human retinoblastoma-binding protein (RbAp46) mRNA, complete cds, IEF 7442 (GB:X72841)	46.86	52.0kDa
217-25	H-X73428	DNA-binding protein inhibitor ID-3	20	17.08
M305 B5	H-X73459	signal recognition particle, subunit 14	15.07	20
M250 D6	H-X73460	ribosomal protein L3, isoform 2, COMPONENT OF THE LARGE SUBUNIT OF CYTOPLASMIC RIBOSOMES	44.44	50.0kDa
M462 D8	H-X74008	Protein phosphatase 1, catalytic subunit, gamma isoform	35.64	46.0kDa
M266 G2	H-X74104	Signal sequence receptor, beta; translocon-associated protein, beta subunit	20.24	27
M266 E7	H-X74262	retinoblastoma binding protein RbAp48	46.86	50.0kDa
H1	H-X74330	DNA primase polypeptide 1 (49kD)	46.31	51
M313 F3	H-X74570	gal beta (1-3/1-4) GlcNAc alpha-2,3 sialyltransferase (GB:X74570)	36.3	46.0kDa
M429 H3	H-X74764	H.sapiens mRNA for receptor protein tyrosine kinase	94.120	98.0kDa

M271 E6	H-X75042	V-rel avian reticuloendotheliosis viral oncogene homolog	68.2	88
M305 G2	H-X75252	phosphatidylethanolamine-binding protein	20.68	30
M302 G1	H-X75593	guanine nucleotide-binding protein rab13	22.44	32.0kDa
166-49	H-X75958	H.sapiens trkB mRNA for protein-tyrosine kinase	55	52.54
C4	H-X76013	H.sapiens QRSHs mRNA for glutaminyl-tRNA synthetase	85.36	85
A2	H-X76029	H.sapiens mRNA for neuromedin U	19.25	20
M305 D5	H-X76228	ATP synthase, H ⁺ transporting, subunit E, vacuolar	24.97	36
M298 F6	H-X76648	glutaredoxin	11.77	11.0kDa
M311 A4	H-X76717	metallothionein II	6.82	14
C4	H-X77533	H.sapiens mRNA for activin type II receptor	56.43	61
H2	H-X77548	H. sapiens cDNA for RFG	67.65	67
169-41	H-X77743	H.sapiens CDK activating kinase mRNA	45	38.1 3
A4	H-X77909	H.sapiens IKBL mRNA	42.02	52
M305 C1	H-X78136	heterogeneous nuclear ribonucleoprotein E2	40.26	40.0kDa
M306 G2	H-X78416	casein, alpha [CSN1]	20.46	33
M271 C2	H-X78678	ketohehexokinase (fructokinase) [KHK], H.sapiens KHK mRNA for ketohehexokinase, clone pHKHK3a	32.89	39
M305 D4	H-X79193	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) [CDK7]	38.17	35
M431 F2	H-X79389	glutathione S-transferase T1	26.51	34.0kDa
M298 C6	H-X79537	glycogenin	30.8	34.0kDa
M440 C1	H-X79865	H.sapiens Mrp17 mRNA	21.89	31.0kDa
M298 F5	H-X80229	protein kinase PKN	52.8	64.0kDa
167-39	H-X80230	H.sapiens mRNA (clone C-2k) mRNA for serine/threonine protein kinase	42	40.99
217-49	H-X80343	H.sapiens p35 mRNA for regulatory subunit of cdk5 kinase	40	33.84
M270 D7	H-X80695	cytochrome oxidase-assembly protein, OXA1, H.sapiens OXA1Hs mRNA	47.96	50
M266 B5	H-X80909	nascent polypeptide-associate complex, alpha	23.76	37.0kDa
M416 D9	H-X80910	Protein phosphatase 1, catalytic subunit, beta isoform	36.08	45.0kDa
E2	H-X81198	Archain	52.03	63
169-6	H-X81817	H.sapiens BAP31 mRNA	32	27.1 3
E4	H-X82018	H.sapiens mRNA for ZID protein	46.75	57
M313 D7	H-X82456	MLN50	28.82	33
A2	H-X82629	H.sapiens mRNA for Mox-2	33.44	42

M236 D1	H-X83006	lipocalin, neutrophil gelatinase associated	21.89	34.0kDa
166-40	H-X83107	H.sapiens Bmx mRNA for cytoplasmic tyrosine kinase	75	74.32
E3	H-X83425	H.sapiens LU gene for Lutheran blood group glycoprotein	69.19	59
C6	H-X83703	H.sapiens mRNA for cytokine inducible nuclear protein	35.2	54
M416 H2	H-X83928	H.sapiens mRNA for transcription factor TFIID subunit TAFII28	23.32	33.0kDa
166-17	H-X85106	H.sapiens mRNA for ribosomal S6 kinase	90	80.70
166-39	H-X85337	H.sapiens mRNA for myosin light chain kinase	110	109.0
D2	H-X85750	H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation	26.29	30
M266 E6	H-X87176	17-beta-hydroxysteroid dehydrogenase, type 4	81.07	65
M297 F2	H-X87689	CLCP	23.21	33.0kDa
M300 A2	H-X87843	cyclin H assembly factor	34.1	47
M271 E3	H-X89750	homeotic protein, TGIF, H.sapiens mRNA for TGIF protein	30.03	32.0kDa
M235 G1	H-X90529	guanine nucleotide-binding protein ragA [RAGA]	34.54	40
M302 E6	H-X90583	translocon-associated protein, delta	19.14	28.0kDa
M306 G1	H-X90872	gp2512	23.65	33
M416 D2	H-X91504	Transcription factor COUP 2 (a.k.a. ARPI)	22.22	32.0kDa
M250 B3	H-X92098	transmembrane protein rnp24	22.22	30
M271 G7	H-X92106	bleomycin hydrolase. PROTECTING NORMAL AND MALIGNANT CELLS FROM BLM TOXICITY.	50.16	55.0kDa
F3	H-X92715	Zinc finger protein 74 (Cos52)	63.03	47
M270 H6	H-X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	70.51	71
H5	H-X92762	H.sapiens mRNA for tafazzins protein	32.23	37
M298 D3	H-X93036	MAT-8	9.68	16.0kDa
M476 A5	H-X93595	H.sapiens mRNA for NK receptor (clone 17.1C)	50.16	56.0kDa
M417 D2	H-X93920	protein tyrosine phosphatase foreskin	41.980	48.0kDa
A5	H-X95592	H.sapiens mRNA for C1D protein	15.62	28
M298 B4	H-X95648	translation initiation factor 2B, alpha subunit	33.66	34.0kDa
F3	H-X95735	H.sapiens mRNA for zyxin 2	63.03	72
M386 B1	H-X96752	L-3-hydroxyacyl-CoA dehydrogenase, SCHAD gene	34.65	45.0kDa

M422 B6	H-X97229	H.sapiens mRNA for NK receptor, clone library 15.212	41.58	48.0kDa
B3	H-X98173	H.sapiens mRNA for MACH-alpha-2 protein	51.15	51
166-14	H-X99325	H.sapiens mRNA for Ste20-like kinase	55	46.9 3
C4	H-X99459	H.sapiens mRNA for sigma 3B protein	21.34	30
M424 C4	H-Y00291	Human hap mRNA encoding a DNA-binding hormone receptor	49.39	59.0kDa
M386 H1	H-Y00345	polyadenylate-binding protein	69.74	70.0kDa
M469 A2	H-Y00630	Plasminogen activator inhibitor, type II (arginine-serpin)	45.76	46.0kDa
M305 E1	H-Y00711	lactate dehydrogenase B	36.85	38.0kDa
H2	H-Y00764	ubiquinol/cytochrome c reductase hinge protein	10.12	33
F5	H-Y07848	H.sapiens EWS, gar22, rrp22 and bam22 genes	36.3	50
M305 G6	H-Z11559	iron-responsive element binding protein 1 [IREB1]	97.9	98
M250 F3	H-Z11566	Pr22 protein , STATHMIN [Homo sapiens], SERVES AS RELAY (VIA PHOSPHORYLATION) FOR DIVERSE SECOND MESSENGER PATHWAYS	16.5	22.0kDa
169-73	H-Z11695	H.sapiens 40 kDa protein kinase related to rat ERK2	50	38.35
M475 C8	H-Z11737	Flavin-containing monooxygenase 4	61.49	70.0kDa
C1	H-Z11898	Octamer binding protein 3	39.71	50
M266 H4	H-Z12830	SSR, alpha subunit	31.57	42.0kDa
A3	H-Z14000	Ring finger protein 1	41.58	50
M300 E1	H-Z14978	actin-related protein	41.47	49
G1	H-Z19002	H.sapiens of PLZF gene encoding kruppel-like zinc finger protein	74.14	84
H1	H-Z21966	POU homeobox protein	33.22	43
M248 G3	H-Z23139	CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR [Homo sapiens]	29.04	34
D3	H-Z26876	ribosomal protein L38	7.81	35
F2	H-Z28339	H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase	35.97	43
M298 B3	H-Z28407	ribosomal protein L8	28.38	39.0kDa
M313 C3	H-Z29330	ubiquitin-conjugating enzyme UbcH2, 23 kDa	20.24	34
M271 F3	H-Z29677	guanine nucleotide-binding protein, ras-related	20.35	28.0kDa
M465 C2	H-Z30425	H.sapiens mRNA for orphan nuclear hormone receptor	38.39	34.0kDa
M302 F5	H-Z31357	cysteine dioxygenase	22.11	31.0kDa

M340 C1	H-Z31695	inositol polyphosphate 5-phosphatase, 43 kDa	40.04	49.0kDa
E3	H-Z32564-2	H.sapiens FRGAMMA mRNA (819bp) for folate receptor	26.84	36
M236 H1	H-Z35227	small G protein, TTF, RAS-RELATED PROTEIN RAC1	21.12	30.0kDa
A10	H-Z35491	H.sapiens mRNA for novel glucocorticoid receptor-associated protein	30.25	60
M440 G5	H-Z37986	H.sapiens mRNA for phenylalkylamine binding protein	25.41	28.0kDa
M297 E2	H-Z47087	cyclin A/cyclin-dependent kinase 2-associated p19	18.04	30.0kDa
F1	H-Z48051	H.sapiens gene for myelin oligodendrocyte glycoprotein (MOG)	27.28	31
A2	H-Z48475	Glucokinase regulator	68.86	70
M302 E4	H-Z48570	sperm zona pellucida-binding protein	16.72	24
M266 A2	H-Z68907	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA, alternatively spliced, partial cds	43.34	45.0kDa
G1	H-Z83850	Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs	45.76	60
H4	H-Z97171	Homo sapiens GLC1A (trabecular meshwork induced glucocorticoid response) gene, exon I, joined CDS	55.55	55
M421 D5	H-Z97632	Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs	28.49	38.0kDa

Example 3 - Construction of Expression Plasmids

The following example illustrates the construction of the expression vectors used in the Examples above. Similar modifications can be made in other vectors for use in creating
5 libraries of expressible gene sequences.

The vector pcDNA3.1/V5-His was obtained from Invitrogen (cat #V810-20) and modified slightly so that it carried an gene sequence for Zeocin™ resistance and lacked the multiple cloning site. A 100µg aliquot was suspended in 200 µl medical irrigation (MI) water. A 5µl aliquot was saved for gel analysis. The remainder was transferred to a 1.7 ml
10 eppendorf tube. The vector was digested with HindIII (400 U) using Promega Buffer E (final volume = 400 µl). The reaction ran 3 hours at 37° C. An aliquot was checked for completeness of digestion by running on an 0.8% agarose gele in 1X TAE, and visualizing with ethidium bromide.

The digested vector was treated with 200 µl phenol/chloroform (pH7.5) according to
15 standard procedures, and the DNA precipitated from the aqueous phase using 1/10 volume 3M NaOAc and 2 volumes 100% EtOH at room temperature, followed by washing with 80% EtOH. The pellet was resuspended in 100 µl MI water.

Two oligonucleotides were added to the resuspended DNA (Topo -H (40 µg) 5'-
(P)AGCTCGCCCTTATTCCGATAGTG (SEQ. ID. NO.: 3), Topo-4 (12 µg) 5'-
20 (P)AGGGCG (SEQ. ID. NO.: 4)), plus 17 µl 10X Promega T4 Ligase buffer. The tube was placed on ice and the volume increased to 170 µl with MI water. The oligos were ligated to the vector using 20U Promega T4 DNA ligase, incubated at 12° C overnight.

The vector was treated with 100 µl phenol/chloroform and the aqueous phase precipitated as described above. The pelleted DNA was resuspended in 150 µl of steril water
25 the redigested with HindIII (17 µl Promega Buffer E, 200 U HindIII - 37° C, 1 hour). The redigested DNA was re-extracted with phenol/chloroform and precipitated with 1/10 volume 3M NaOAc and 7/10 volume isopropanol, then washed with 80% EtOH.

The pelleted DNA was resuspended in 82 µl TE buffer (10 mM Tris, pH 8.0, 1 mM EDTA, pH 8.0). A 2 µl aliquot was used to check the foregoing procedure using agorose gel
30 electrophoresis as described above. The remaining 80 µl was transferred to a Falcon tube and

mixed with 16 µg Topo-5 oligonucleotide (5'-(P)CAACACTATCGGAATA (SEQ. ID. NO.: 5). To this mixture was added 190 µl NEB Restriction Buffer #1 (room temperature). The total reaction mixture was adjusted to 1.9 mls with MI water. Vaccinia Topoisomerase I enzyme was added (80 µg) and the reaction tube placed in a 37° C water bath for 15 minutes.

- 5 After 15 minutes, 200 µl of room temperature Topo-10X stop buffer was added (100 mM Tris 7.4, 110 mM EDTA, bromophenol blue). The entire volume was loaded onto an agarose gell (1.2 gr agarose/ 130 mls 1X TAE) and run at 70 volts until the bromophenol blue dye had run down about 1/2 in (volume in the loading well was kept constant by the addition of 1X TE). The voltage was reversed for 90 seconds. The contents of the loading
- 10 well were transfered to a 15 ml Falcon tube and placed on ice. 2 mls of cold Topo-2X Wash Buffer (60 mM Tris 7.4, 1 mM EDTA, 4 mM dithiothreitol (DTT), 200 µg/ml bovine serum albumin (BSA)) was added and the volume then adjusted to 4 mls with cold Topo-1X Enzyme Dilution Buffer (50% glycerol, 50 mM Tris 7.4, 1 mM EDTA, 2 mM DTT, 0.1% Triton X-100, 100 µg.ml BSA) plus 4 mls Topo-Glycerol mix (90% glycerol, 10% 50 mM
- 15 TE pH 7.4, 0.1% Triton X-100) and stored until needed.

A similar procedure was used to make Topo-adapted pYES2 (Invitrogen cat # V825-20).

- While the foregoing has been presented with reference to particular embodiments of the invention, it will be appreciated by those skilled in the art that
- 20 changes in these embodiments may be made without departing from the principles and spirit of the invention, the scope of which is defined by the appended claims.

That which is claimed is:

1. A nucleic acid construct comprising 1) a gene sequence encoding a protein listed in Table 1 or an ORF listed in Table 2 and 2) an expression vector.
2. A nucleic acid construct according to claim 1 wherein the expression vector comprises one or more elements selected from: a promoter-enhancer sequence, a selection marker sequence, an origin of replication, an epitope-tag encoding sequence or an affinity purification-tag encoding sequence.
3. A nucleic acid construct according to claim 2 wherein the promoter-enhancer sequence is the T7 promoter, gall promoter, metallothionein promoter, AraC promoter, or CMV promoter-enhancer.
4. A nucleic acid construct according to claim 2 wherein the selection marker sequence encodes an antibiotic resistance gene.
5. A nucleic acid construct according to claim 2 wherein the epitope-tag sequence encodes V5, the peptide Phe-His-His-Thr-Thr, hemagglutinin, or glutathione-S-transferase.
6. A nucleic acid construct according to claim 2 wherein the affinity purification-tag sequence encodes a polyamino acid sequence or a polypeptide.
7. A nucleic acid construct according to claim 6 wherein said polyamino acid sequence is polyhistidine.
8. A nucleic acid construct according to claim 6 wherein said polypeptide is chitin binding domain or glutathione-S-transferase.
9. A nucleic acid construct according to claim 6 wherein said polypeptide encoding sequence includes an intein encoding sequence.

10. A nucleic acid construct according to claim 1 wherein the expression vector is a eukaryotic expression vector or a prokaryotic expression vector.

11. A nucleic acid construct according to claim 10 wherein the eukaryotic expression vector is pYES2/GS, pMT, pIND, or pcDNA3.1/GS.

12. A nucleic acid construct according to claim 1 wherein the protein is selected from the group of proteins listed as number 1 through number 20 in Table 1.

13. A nucleic acid construct according to claim 1 wherein the protein is selected from the group of proteins listed as number 21 through number 40 in Table 1.

14. A nucleic acid construct according to claim 1 wherein the protein is selected from the group of proteins listed as number 41 through number 60 in Table 1.

15. A nucleic acid construct according to claim 1 wherein the protein selected from the group of proteins listed as number 61 through number 80 in Table 1.

16. A nucleic acid construct according to claim 1 wherein the protein is selected from the group of proteins listed as number 81 through number 100 in Table 1.

17. A nucleic acid construct according to claim 1 wherein the protein is selected from the group of proteins listed as number 101 through number 118 in Table 1.

18. A nucleic acid construct according to claim 1 wherein the construct comprises an ORF listed in Table 2.

19. A recombinant cell comprising a nucleic acid construct of claim 1.

20. A recombinant cell of claim 19 wherein the cell is a non-adherent cell.

21. A recombinant cell of claim 20 wherein the non-adherent cell is a bacterial cell, a yeast cell, plant cell, an insect cell or a mammalian cell.

22. A recombinant cell of claim 21 wherein the mammalian cell is CHO or 32D.
23. A method of producing recombinant protein, said method comprising:
(a) growing recombinant cells comprising a nucleic acid construct of claim 1 under suitable growth conditions; and
(b) isolating the recombinant protein expressed thereby.
24. A method according to claim 23 wherein the nucleic acid construct comprises an epitope-tag encoding sequence and the isolation step utilizes an antibody specific for said epitope-tag.
25. A method according to claim 24 wherein the nucleic acid construct comprises a polyamino acid encoding sequence and the isolation step utilizes a resin comprising a polyamino acid binding substance.
26. A method according to claim 23 wherein the nucleic acid construct comprises a polypeptide encoding sequence and the isolation step utilizes a resin comprising a polypeptide binding substance.
27. A method according to claim 25 wherein the polyamino acid is polyhistidine and the polyamino binding resin is nickel-charged agarose resin.
28. A method according to claim 26 wherein the polypeptide is chitin binding domain and the resin comprises chitin-Sepharose.
29. A kit comprising a plurality of expression constructs, wherein each expression construct comprises a gene sequence encoding a protein listed in Table 1 and an expression vector.
30. A kit according to claim 29 wherein the expression vector is pYES2/GS or pcDNA3.1/GS.

31. A kit comprising a plurality of recombinant cells, wherein each cell comprises a gene sequence encoding a protein listed in Table 1 and an expression vector.

32. A kit according to claim 31 wherein the expression vector is pYES2/GS or pcDNA3.1/GS and the recombinant cell is a yeast cell or a mammalian cell.

33. A kit according to claim 32 wherein the mammalian cell is a CHO cell.

34. A kit comprising a plurality of expression constructs, wherein each expression construct comprises an ORF listed in Table 2 and an expression vector.

35. A kit according to claim 34 wherein the expression vector is pYES2/GS or pcDNA3.1/GS.

36. A kit comprising a plurality of recombinant cells, wherein each cell comprises an ORF listed in Table 2 and an expression vector.

37. A kit according to claim 36 wherein the expression vector is pYES2/GS or pcDNA3.1/GS and the recombinant cell is a yeast cell or a mammalian cell.

38. A kit comprising one or more of: expression construct(s) comprising a gene sequence encoding a protein listed in Table 1 and an expression vector; recombinant cells comprising an expression construct comprising a gene sequence encoding a protein listed in Table 1 and an expression vector; and an isolated protein
5 listed in Table 1 or an antibody specific for said isolated protein.

39. A binding partner of an expressed gene product of a gene sequence listed in Table 1.

40. A binding partner of an expressed gene product of a gene sequence listed in Table 2.

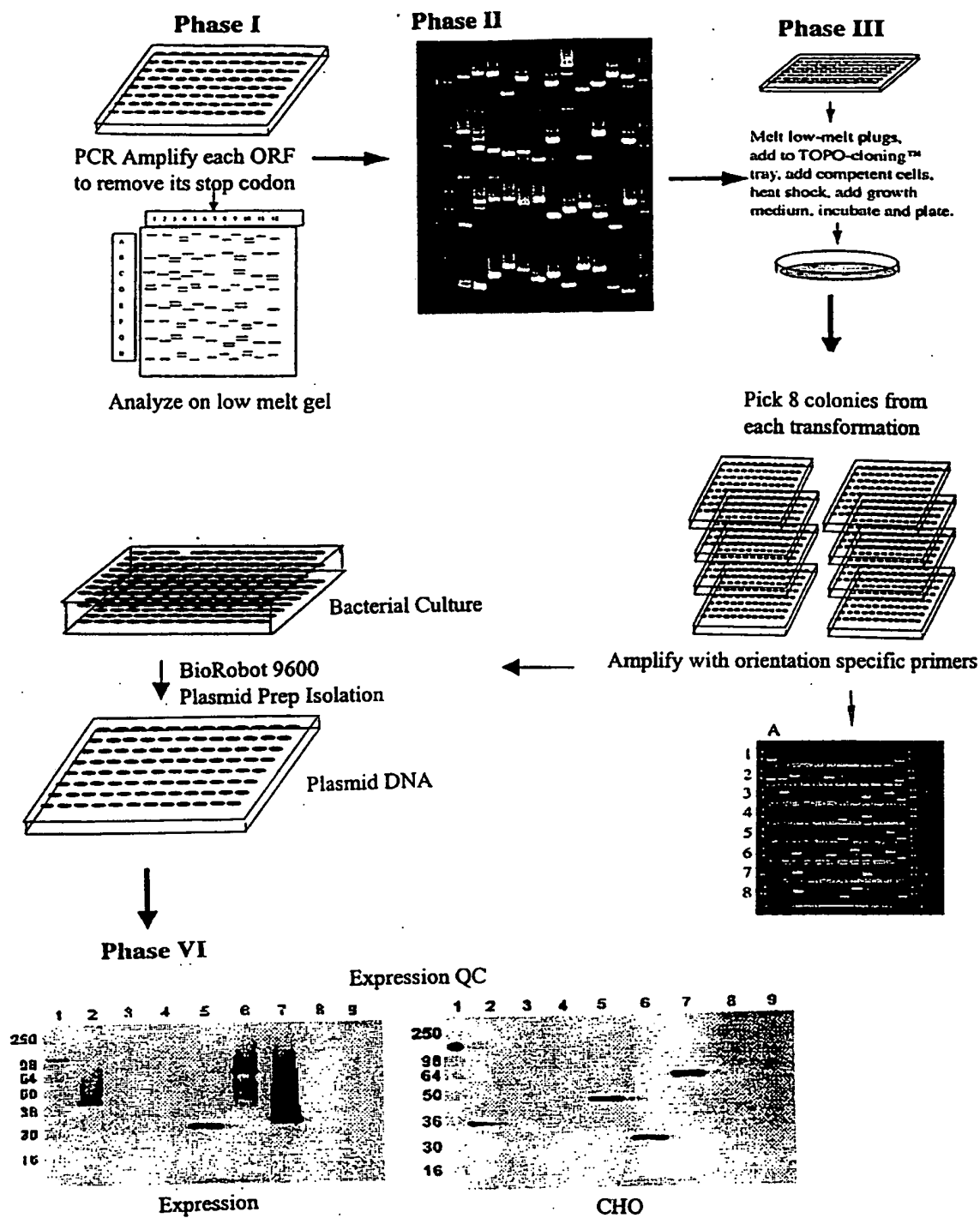


Figure 1

INTERNATIONAL SEARCH REPORT

 International application No.
PCT/US99/07334
A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 252.3, 254.11, 320.1, 325; 536/23.1, 23.2, 23.4, 23.7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. L05146, 'Saccharomyces cerevisiae chromosome I left arm sequence', entire record, 05 March 1998.	1-11, 18-38
X	Database GenBank, US National Library of Medicine, (Bethesda, MD, USA), No. L22015, 'Saccharomyces cerevisiae chromosome I centromere and right arm sequence', entire record, 05 March 1998.	1-11, 18-38

☐ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

21 JUNE 1999

Date of mailing of the international search report

04 AUG 1999

 Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/07334

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 12-17
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Table 1 does not list any proteins numbered as 1-118.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11, 18-38

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/07334

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C07H 21/00; C12N 1/19, 1/21, 15/31, 15/32, 15/62, 15/63, 15/70, 15/74, 15/79, 15/81

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

435/69.1, 252.3, 254.11, 320.1, 325; 536/23.1, 23.2, 23.4, 23.7

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

GENBANK, MEDLINE, EMBASE, BIOSIS, CAPLUS, SCISEARCH

search terms: YAL003W, YAL005C, YAL007C, YAL009W, YAL012, YAL013W, YAL014C, YAL015C, YAL016W, YAL020C, cerevisiae, FUN28, TPD3, protein phosphatase 2A, PP2A, subunit A, DEP1

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups I-MCCXV, claim(s) 1-11, 18-38, drawn to expression vector comprising coding sequence for one of the 2937 or 1947 different proteins listed in Tables 1 or 2, respectively, the protein encoded (claim 38) and a method for using the vectors to make the protein. Group I pertains to the first ten (10) entries in Table 1. Each succeeding group pertains to each succeeding four entries from Table 1 then Table 2.

Groups MCCXVI-VMIC, claim(s) 38, drawn to antibodies to one of the 2937 or 1947 different proteins listed in Tables 1 or 2, respectively. Group MCCXVI pertains to the first entry in Table 1. Each succeeding group pertains to each succeeding entry from Table 1 then Table 2.

Group VMC-MVXXXVI, claim(s) 39, drawn to binding partner for one of the 2937 different proteins listed in Tables 1. Group VMC pertains to the first entry in Table 1. Each succeeding group pertains to each succeeding entry from Table 1.

Groups MVXXXVII-XCMLXXXIII, claim 40, drawn to binding partner for one of the 1947 different proteins listed in Tables 2. Group MVXXXVII pertains to the first entry in Table 2. Each succeeding group pertains to each succeeding entry from Table 2.

The inventions listed as Groups I-XCMLXXXIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Tables 1 and 2 list 4884 different independent proteins, and as such represent 4884 different independent inventions. The corresponding vectors and proteins of Groups I-MCCXV, antibodies of Groups MCCXVI-VMIC, and binding partners of groups VMC-XCMLXXXIII are physically, biochemically and biologically different compounds. 37 CFR 1.475(b) does not provide for unity of invention of more than 1 product as a combination of inventions having unity of invention. However, with respect to groups drawn to independent polynucleotides, in this case vectors, or alternate methods of using same recited in the alternative, in accordance with 1192 O.G. 68 (19 November 1966) applicant is entitled to an initial search of inventions pertaining to the first ten independent polynucleotides recited, and may elect to pay an additional fee for each search of up to four additional independent polynucleotides. With respect to groups pertaining to independent polypeptides, such as corresponding antibodies or binding partners to the independent polypeptides, each product is an additional invention. An additional fee must be paid for search of each additional invention relating to antibodies or binding partners for the proteins.